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                GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    August 17, 2005, 22:08:26 ; Search time 243 Seconds
                                       (without alignments)
                                       8073.645 Million cell updates/sec

Title:           US-10-735-577-16
Perfect score:   1199
Sequence:        1 ggaactaaaaagaactta..........cgggcttcccgcgcccaccgg 1199

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters:   2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
c 1	601	50.1	649	4	US-09-461-912A-36	Sequence 36, Appl
c 2	557	46.5	579	4	US-09-461-912A-24	Sequence 24, Appl
c 3	523	43.6	582	4	US-09-513-999C-14898	Sequence 14898, A
c 4	485.2	40.5	2016	4	US-10-000-489-1	Sequence 1, Appli
c 5	329.8	27.5	600	3	US-09-399-913-64	Sequence 64, Appl
c 6	329.8	27.5	600	4	US-09-350-614-64	Sequence 64, Appl
c 7	328.4	27.4	570	4	US-09-461-912A-23	Sequence 23, Appl
c 8	164.8	13.7	276	3	US-09-313-294A-4020	Sequence 4020, Ap
c 9	164.8	13.7	509	4	US-09-385-982-150	Sequence 150, App
c 10	101	8.4	191	4	US-09-680-420A-21	Sequence 21, Appl
c 11	85.8	7.2	522	4	US-09-774-528-414	Sequence 414, App
c 12	75.2	6.3	592	4	US-09-949-016-5370	Sequence 5370, Ap
c 13	71.2	5.9	434	4	US-09-949-016-4686	Sequence 4686, Ap
c 14	71.2	5.9	439	4	US-09-814-915A-87	Sequence 87, Appl
c 15	71.2	5.9	860	4	US-09-919-172-101	Sequence 101, App
c 16	71.2	5.9	860	4	US-09-976-594-466	Sequence 466, App
c 17	69	5.8	205	4	US-09-513-999C-14895	Sequence 14895, A
c 18	65.2	5.4	1081	4	US-09-566-921-119	Sequence 119, App
c 19	63.6	5.3	962	4	US-09-919-039-183	Sequence 183, App
c 20	62.2	5.2	279	4	US-09-513-999C-1413	Sequence 1413, Ap
c 21	54.4	4.5	2592	4	US-09-949-016-2162	Sequence 2162, Ap
c 22	54.4	4.5	43690	4	US-09-949-016-13904	Sequence 13904, A
c 23	54.2	4.5	421	3	US-09-643-597-308	Sequence 308, App
c 24	54.2	4.5	421	4	US-09-480-884A-308	Sequence 308, App
c 25	54.2	4.5	421	4	US-09-542-615A-308	Sequence 308, App
c 26	54.2	4.5	421	4	US-09-606-421B-308	Sequence 308, App
c 27	54.2	4.5	421	4	US-09-630-940B-308	Sequence 308, App
c 28	54.2	4.5	527	3	US-09-370-838-281	Sequence 281, App
c 29	54.2	4.5	527	1	US-09-854-133-281	Sequence 281, Appl
c 30	54.2	4.5	579	1	US-08-190-560-3	Sequence 3, Appli
c 31	54.2	4.5	579	1	US-08-469-277-3	Sequence 3, Appli
c 32	54.2	4.5	579	2	US-08-468-946-3	Sequence 3, Appli
c 33	54.2	4.5	579	2	US-08-468-942-3	Sequence 3, Appli
c 34	54.2	4.5	579	4	US-09-298-625-3	Sequence 3, Appli
c 35	54	4.5	86380	1	US-09-949-016-14837	Sequence 14837, A
c 36	53.2	4.4	303	1	US-09-190-560-1	Sequence 1, Appli
c 37	53.2	4.4	303	1	US-08-469-277-1	Sequence 1, Appli
c 38	53.2	4.4	303	2	US-08-468-946-1	Sequence 1, Appli
c 39	53.2	4.4	303	2	US-08-468-942-1	Sequence 1, Appli
c 40	53.2	4.4	303	4	US-09-298-625-1	Sequence 1, Appli
c 41	52.8	4.4	452	1	US-07-662-198B-1	Sequence 1, Appli
c 42	52.8	4.4	452	1	US-08-322-742-1	Sequence 1, Appli
c 43	52.6	4.4	392	4	US-09-702-705-1585	Sequence 1585, Ap
c 44	52.6	4.4	392	4	US-09-735-457-1585	Sequence 1585, Ap
c 45	52.6	4.4	392	4	US-09-614-124B-1585	Sequence 1585, Ap

ALIGNMENTS

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RESULT 1
US-09-461-912A-36/c
; Sequence 36, Application US/09461912A
; Patent No. 6709855
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Lawrence A.
;  APPLICANT: White, R. Tyler
;  APPLICANT: Damm, Deborah L.
;  APPLICANT: Lewicki, John A.
;  TITLE OF INVENTION: Methods for detection and use of
;  TITLE OF INVENTION: differentially expressed genes in disease states
;  FILE REFERENCE: SCIOS.011A
;  CURRENT APPLICATION NUMBER: US/09/461,912A
;  CURRENT FILING DATE: 1999-12-15
;  PRIOR APPLICATION NUMBER: US 60/113,008
;  PRIOR FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
US-09-461-912A-36
;  SEQ ID NO 36
;  LENGTH: 649
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (113)...(405)
US-09-461-912A-36

Query Match             50.1%;  Score 601;  DB 4;  Length 649;
Best Local Similarity   99.7%;  Pred. No. 2.9e-148;
Matches  623;  Mismatches   0;  Conservative   0;  Indels   2;  Gaps   2;

Qy    1 GGAACTAAAAAGAACTTATTTATTTGAGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db  649 GGAACTAAAAAGAACTTATTTATTTGAGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  589 AAGCTTATCTGGTATTTAACTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCGTGTGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCGTGTGG 470

Qy  181 GCAGATTCCTTAAGCGACACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  469 GCAGATTCCTTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy  241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  410 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 351
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Right column:

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Qy  301  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  360
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Db  280  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  221

Qy  361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  220  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  161

Qy  421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTTATCCCCA  480
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Db  160  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTTATCCCCA  101

Qy  481  GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  100  GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT  41

Qy  541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGCGGAC  581
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Db   40  TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGGCGGAC  1
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RESULT 3
US-09-513-999C-14898/c
; Sequence 14898, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14898
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 114
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 117
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 126
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 140
; OTHER INFORMATION: r=a or g
; US-09-513-999C-14898

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Query Match             43.6%;  Score 523;  DB 4;  Length 582;
Best Local Similarity   97.9%;  Pred. No. 9.6e-128;
Matches  547;  Conservative  4;  Mismatches  4;  Indels  4;  Gaps  2;

Qy   30  GGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTTATCTGGTATTTAACTTTCTTTC   89
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  582  GGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTTATCTGGTATTTAACTTTCTTTC  523
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Left column:

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Qy  601  CTGGACGCGGGGGCGGAGGAGGCGAGC  625
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Db   51  CTGGACGCGGGGGCGGAGGAGGCGAGC  27
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RESULT 2
US-09-461-912A-24/c
; Sequence 24, Application US/09461912A
; Patent No. 6709855
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence A.
; APPLICANT: White, R. Tyler
; APPLICANT: Damm, Deborah L.
; APPLICANT: Lewicki, John A.
; TITLE OF INVENTION: Methods for detection and use of
; TITLE OF INVENTION: differentially expressed genes in disease states
; FILE REFERENCE: SCIOS.011A
; CURRENT APPLICATION NUMBER: US/09/461,912A
; CURRENT FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,008
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-461-912A-24

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Query Match             46.5%;  Score 557;  DB 4;  Length 579;
Best Local Similarity   99.7%;  Pred. No. 1.1e-136;
Matches  579;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy    1  GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA   60
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Db  579  GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  520

Qy   61  AAGCTTATCTGGTATTTAACTTTCTTTCTTCTTCTCTCGCTTGTCAAATGAGAGTTGATTTTATT  120
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Db  519  AAGCTTATCTGGTATTTAACTTTCTTTCTTCTTCTCTCGCTTGTCAAATGAGAGTTGATTTTATT  460

Qy  121  TTTACATTTGCTAAGTAGTGTCCTGATCGTCCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  459  TTTACATTTGCTAAGTAGTGTCCTGATCGTCCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  400

Qy  181  GCAGATTCCTTAAGGCACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  399  GCAGATTCCTTAAGGCACCCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  341

Qy  241  TCTGCCTACTTCTTTCCCTTCGCTTGCTCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  340  TCTGCCTACTTCTTTCCCTTCGCTTGCTCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  281
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;  NAME/KEY: polyA_signal
;  LOCATION: 1965..1970
;  NAME/KEY: polyA_site
;  LOCATION: 2001..2016
US-10-000-489-1

Query Match             40.5%;  Score 485.2;  DB 4;  Length 2016;
Best Local Similarity   94.7%;  Pred. No. 1.5e-117;
Matches  502;  Conservative   0;  Mismatches  28;  Indels   0;  Gaps   0;

Qy       73 TATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 132
            || ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2012 TTTTTTTTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTTATTTTTACATTTGCT 1953

Qy      133 AAGTGTCCTGATCTGCTCATGAAATCCTTATGGGGGAAGCTGTGGGGCAGATTCCTTA 192
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1952 AAGTGTCCTGATCTGCTCATGAAATCCTTATGGGGGAAGCTGTGGGGCAGATTCCTTA 1893

Qy      193 AGCGACCCTTGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 252
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1892 AGCGACCCTTGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 1833

Qy      253 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCCCGCA 312
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1832 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCCCGCA 1773

Qy      313 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTTTGCCATCTCTC 372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1772 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTTTGCCATCTCTC 1713

Qy      373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTCCAAAAATCCAGGGAACTCCTTT 432
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1712 ATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy      433 TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 492
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1652 TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 1593

Qy      493 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 552
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1592 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 1533

Qy      553 GTTGAAGCCTTGGCCGAGGCGGCGGCGACGCTCGGCGAGCTGGGCGAGCT 602
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Db     1532 GTTGAAGCCACCAGAGGCTCAGTGCGAGGTCTGGGCAGGCAAGAAAAGGT 1483
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RESULT 5
US-09-399-913-64/c
; Sequence 64, Application US/09399913
; Patent No. 6361971
GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: Betty, Maria
; APPLICANT: Ling, Huai-Ping
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070CP2
; CURRENT APPLICATION NUMBER: US/09/399,913
; CURRENT FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: USSN 09/350,614
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 09/350,874
; EARLIER FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 73

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Qy       90 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCTAAGTGTCCTGATCTGCT 149
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      522 TCTGCTTGTCAAATGAGAGTTAGATTTTTATTTTTACATTTGCTAAGTGTCCTGATCTGCT 463

Qy      150 CATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATTCCTTAAGCGACCCTTGGGACA 209
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      462 CATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATTCCTTAAGCGACCCTTT--GACA 405

Qy      210 ACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTCTCTTCTGCTTCAT 269
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      404 ACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTTCTCTTCTGCTTCAT 345

Qy      270 GTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCT 329
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      344 GTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCT 285

Qy      330 CTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTTGTCCACAGC 389
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      284 CTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTTGTCCACAGC 225

Qy      390 CAGAGGGTCTTTTTGATTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAG 449
            |||||||||   |||||||||||||||||||||||||||||||||||||||||||||||
Db      224 CAGAGGGTC--TTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAG 167

Qy      450 GTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGGT 509
            |||||||||||||||||||||||||| ||:|||||||||||||:|:|||||||||||||
Db      166 GTCCTCCTTTGTTAAGTAGCCTTTATYCCCAGCGAATTGYGAAATGTAMACRTCATGGT 107

Qy      510 TTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGTCCGTTGAAGCCTTGGCCGA 569
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      106 TTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGTCCGTTGAAGCCTTGGCCGA 47

Qy      570 GGGCGGCGGCGACGCTGGGC 588
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Db       46 GGCGCGGCGGGCGTGCGC 28
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RESULT 4
US-10-000-489-1/c
; Sequence 1, Application US/10000489
; Patent No. 6794363
GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREFOR
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
SEQ ID NO 1
; LENGTH: 2016
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..1434
; NAME/KEY: CDS
; LOCATION: 1435..1836
; NAME/KEY: 3'UTR
; LOCATION: 1837..2016

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;   SOFTWARE: PatentIn Ver. 2.0                                          ;   EARLIER FILING DATE: 1998-11-25
;   SEQ ID NO 64                                                         ;   EARLIER APPLICATION NUMBER: USSN 60/109,333
;   LENGTH: 600                                                          ;   EARLIER FILING DATE: 1998-11-20
;   TYPE: DNA                                                            ;   NUMBER OF SEQ ID NOS: 72
;   ORGANISM: Rattus sp.                                                 ;   SOFTWARE: PatentIn Ver. 2.0
;   FEATURE:                                                             ;   SEQ ID NO 64
;   NAME/KEY: CDS                                                        ;   LENGTH: 600
;   LOCATION: (52)..(336)                                               ;   TYPE: DNA
US-09-399-913-64                                                         ;   ORGANISM: Rattus sp.
                                                                        ;   FEATURE:
                                                                        ;   NAME/KEY: CDS
                                                                        ;   LOCATION: (52)..(336)
                                                                       US-09-350-614-64

Query Match      27.5%;    Score 329.8;  DB 3;   Length 600;            Query Match      27.5%;    Score 329.8;  DB 4;   Length 600;
Best Local Similarity 77.8%;  Pred. No. 7.3e-77;                        Best Local Similarity 77.8%;  Pred. No. 7.3e-77;
Matches 458;  Conservative  0;  Mismatches 107;  Indels 24;  Gaps 4;    Matches 458;  Conservative  0;  Mismatches 107;  Indels 24;  Gaps 4;

Qy    7  AAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAATCAAAAGCTT 66    Qy    7  AAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAATCAAAAGCTT 66
         |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||            |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  569  AAAAAAAGAACTTTCTTTATTGAGGGCAACCGGATGCAAACAATATAAAACTCGAAAGCTC 510   Db  569  AAAAAAAGAACTTTCTTTATTGAGGGCAACCGGATGCAAACAATATAAAACTCGAAAGCTC 510

Qy   67  ATCTGGTAT----TTAACTTTCTTTCTTTCTTTCTTTCTTTCTTTAGATTTATTTT 122     Qy   67  ATCTGGTAT----TTAACTTTCTTTCTTTCTTTCTTTCTTTCTTTAGATTTATTTT 122
         |||||||||        ||||||| ||||||||||||||||||| |||||||||||||           |||||||||        ||||||| |||||||||||||||||||| |||||||||||||
Db  509  CTCTGTCATTGGATTAACTTTCTTTCTTTCTTTCTTTGTCATGGGGAAGCTGTGGGGC 450   Db  509  CTCTGTCATTGGATTAACTTTCTTTCTTTCTTTCTTTGTCATGGGGAAGCTGTGGGGC 450

Qy  123  TACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGGC 182    Qy  123  TACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGGC 182
         ||||||||||||||||||||||||||||                                         ||||||||||||||||||||||||||||
Db  449  CACATTTCCTAAGGGTCCTGATCTGCTCA----------CAGGAAGCAGTGGGGC 405     Db  449  CACATTTCCTAAGGGTCCTGATCTGCTCA----------CAGGAAGCAGTGGGGC 405

Qy  183  AGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGGAGCTGCTCATTTC 242     Qy  183  AGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGGAGCTGCTCATTTC 242
         |||| |||||||| ||||||||||||||||||| ||||||||||||  ||||||||||           |||| |||||||| ||||||||||||||||||| ||||||||||||  ||||||||||
Db  404  AGATTCCTCAGTGACCCCCATGGGACCATCAAGGTGTGGGTACCAGGGC----T 349     Db  404  AGATTCCTCAGTGACCCCCATGGGACCATCAAGGTGTGGGTACCAGGGC----T 349

Qy  243  TGCCTACTTCTTTCCCTTCTGAAGCCCACTTTGCCATCTCTACACTGGTC 302          Qy  243  TGCCTACTTCTTTCCCTTCTGAAGCCCACTTTGCCATCTCTACACTGGTC 302
         ||||||||||| ||||||||||||||||||||||| ||||||||||||||                    ||||||||||| ||||||||||||||||||||||| ||||||||||||||
Db  348  CCAGTTGGCCTACTTCTTTCTCGGAAGCTCGGAAGCTCCACTTTGCCACTGGTC 289        Db  348  CCAGTTGGCCTACTTCTTTCTCGGAAGCTCGGAAGCTCCACTTTGCCACTGGTC 289

Qy  303  GAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGAAGCTCTGGAAATCCAGG 362         Qy  303  GAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGAAGCTCTGGAAATCCAGG 362
         |||||||||||||||||||||||||||||||| |||||||||| ||||||||||               |||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Db  288  GAGGCCCGCCACTAGTGATAGAAAGCTCTGGAAGCTCTGGAAGCTCGGCACTGGTC 229     Db  288  GAGGCCCGCCACTAGTGATAGAAAGCTCTGGAAGCTCTGGAAGCTCGGCACTGGTC 229

Qy  363  CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGTTGTAGCCTTATCCCCAGC 422  Qy  363  CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGTTGTAGCCTTATCCCCAGC 422
         |||||||||||||||||||| |||||||||||||||||| |||||||||||||||||||          |||||||||||||||||||| |||||||||||||||||| |||||||||||||||||||
Db  228  CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTTGTCAAGTAGTTTTTTCCCCTGC 169  Db  228  CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTTGTCAAGTAGTTTTTTCCCCTGC 169

Qy  423  GAACTCCTTTGTGAAATGTAAACATCATGGTGTTCCATTTGAAGTGGCATTTT 482         Qy  423  GAACTCCTTTGTGAAATGTAAACATCATGGTGTTCCATTTGAAGTGGCATTTT 482
         ||||||||||| |||||||||||||||||||| ||||||||||||||||                     ||||||||||| |||||||||||||||||||| ||||||||||||||||
Db  168  GAACTCCCTTTCCATGGACATCATGGTTTCCATTTGCAAGTAGTTTTTTTCCCCTGC 109     Db  168  GAACTCCCTTTCCATGGACATCATGGTTTCCATTTGCAAGTAGTTTTTTTCCCCTGC 109

Qy  483  GAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTT 542             Qy  483  GAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTT 542
         ||||| ||||||||||| ||||||||| |||||||||||||                              ||||| ||||||||||| ||||||||| |||||||||||||
Db  108  AAACCTGTGAAATGTAAGCATCATGGTTTCCATTTGGGATGGCATTTT 49             Db  108  AAACCTGTGAAATGTAAGCATCATGGTTTCCATTTGGGATGGCATTTT 49

Qy  543  GGTGTGGTCCGTTGAAGCCTTCGGCCCGAGGCGCCGGACGCGTGGGCGAG 591         Qy  543  GGTGTGGTCCGTTGAAGCCTTCGGCCCGAGGCGCCGGACGCGTGGGCGAG 591
         ||||||| |||||||||||      ||||||||||| |||||||||||                      ||||||| |||||||||||      ||||||||||| |||||||||||
Db   48  GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCAGTCTTTGGAAG 1            Db   48  GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCAGTCTTTGGAAG 1
```

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RESULT 6                                                                RESULT 7
US-09-350-614-64/c                                                      US-09-461-912A-23/c
;  Sequence 64, Application US/09350614                                  ;  Sequence 23, Application US/09461912A
;  Patent No. 6689581                                                    ;  Patent No. 6709855
;  GENERAL INFORMATION:                                                  ;  GENERAL INFORMATION:
;     APPLICANT: Rhodes, Kenneth                                         ;     APPLICANT: Stanton, Lawrence A.
;     APPLICANT: Betty, Maria                                            ;     APPLICANT: White, R. Tyler
;     APPLICANT: Ling, Huai-Ping                                         ;     APPLICANT: Damm, Deborah L.
;     APPLICANT: An, Wenqian                                             ;     APPLICANT: Lewicki, John A.
;     TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR;     TITLE OF INVENTION: Methods for detection and use of
;     FILE REFERENCE: MNI-070CP                                          ;     TITLE OF INVENTION: differentially expressed genes in disease states
;     CURRENT APPLICATION NUMBER: US/09/350,614                          ;     FILE REFERENCE: SCIOS.011A
;     CURRENT FILING DATE: 1999-07-09                                    ;     CURRENT APPLICATION NUMBER: US/09/461,912A
;     EARLIER APPLICATION NUMBER: USSN 09/298,731                        ;     CURRENT FILING DATE: 1999-12-15
;     EARLIER FILING DATE: 1999-04-23
;     EARLIER APPLICATION NUMBER: USSN 60/110,277
;     EARLIER FILING DATE: 1998-11-30
;     EARLIER APPLICATION NUMBER: USSN 60/110,033
```

; PRIOR APPLICATION NUMBER: US 60/113,008
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-461-912A-23

Query Match   27.4%; Score 328.4; DB 4; Length 570;
Best Local Similarity   78.4%; Pred. No. 1.7e-76;
Matches   453; Conservative   0; Mismatches 101; Indels   24; Gaps   4;

Qy   7 AAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTT   66
             |||||| ||||||| || |||||||||||||||||||| ||||||||||||| |||||
Db   561 AAAAAAGAACTTTCTTTATTGAGGGCAACCGGATGCAAACAATATAAAACTCGAAAGCTC   502

Qy   67 ATCTGGTAT----TTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT   122
             | ||||| |||||| | ||||| |||||||||||||||||| |||| ||||| ||||
Db   501 CTCTGTCATTGGATTAACTTTTCTTTCTCTGCTTGTCGAATTGGAGTTGGATGTTATTTG   442

Qy   123 TACATTTGCTAAGTGTCCTGATCTGCTCATGCTTCATGCTCTATGGGGAAGCTGTGGGGC   182
             ||||||||||||||||||||||||||||||| ||||| ||| |||| |||||||||||
Db   441 CACATTTCCTAAGGGTCCGTGATCTGCTCA----------CAGGAAGCAGTGGGGC   397

Qy   183 AGATTCCTAAGCAGACCCCTTTGGACAACTCTTATCAGGGAGGAGCCAACTGCTCATTTC   242
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   396 AGATTCCTCAGTTGACCCTCAGTTGGGGTGGGCATGTGGGGTACCAGGGC----T   341

Qy   243 TGCCTACTTCTTTCCCTTCTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGGT   302
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   340 CCAGTTGGCCTACTTCTTTCCCTTCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGAT   281

Qy   303 GAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTCTGGAAGCCATCTCTACACTGGTC   362
             ||||||||| ||| |||||||||||||||||||||||||| ||||||||||||||||||||
Db   280 GAGCCCGCCGCCACTAGTGATAGAAAGCTCTGGAAGCCCACTTCTTCCAATCTCGGCACTGGTC   221

Qy   363 CAGGTCCTCATTATTTTGTCCACGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG   422
             |||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   220 CAGGTCTTTCATTATTTTGTCCACGCCAGAGGGTCCTTTTGATTTTCCAAAAAACCCAGG   161

Qy   423 GAACTCCTTTCCATGAGTACTCCAGGTCCTCCCTTTGTGTAAGTAGCCTTTATCCCCAGC   482
             ||||||||||||||||||||||||||||||||| ||||||| ||| |||||||||||||
Db   160 GAACTCCCTTTCCATGAGCACTCTCAGGTCCTCCAGTTTGTCAAGTAGTTTTTTTCCCCTGC   101

Qy   483 GAATTTGTGAAATGTAAACATCATGTTTCCATGGCCGTGTTCCATTTGAGATGGCATTTT   542
             | ||||||||||||| |||||||||| |||||||||||||| ||||||||||||||| ||
Db   100 AAACCTGTGAAATGTAAGCATCATGTTTCCATGGCATGCTCCATTTGGGATGGCATTTTT   41

Qy   543 GGTGTGGTCCGTTGAAGCCTTGGCCCGGCGCGGCGCGGA   580
             |||||| ||||||||||||| |||||| ||| ||||||
Db   40 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCA   4

RESULT 8
US-09-313-294A-4020/c
; Sequence 4020, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4020
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays

; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 70034754B H1
; NAME/KEY: unsure
; LOCATION: 70
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4020

Query Match   13.7%; Score 164.8; DB 4; Length 276;
Best Local Similarity   79.9%; Pred. No. 1.4e-33;
Matches   218; Conservative   0; Mismatches   53; Indels   2; Gaps   2;

Qy   320 AAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTT   379
             | |||||||||||||||||||||||||-||||||||||||||||||||||||||||||||
Db   276 ATAGAAAGCTCTGGAAGCCCACTTT-CCATCTCGGCACTGGTCCAGGTCTTTCATTATTT   218

Qy   380 TGTCCACAGCCAGAGGGTCTTTTG-ATTTTCCAAAAATCCAGGGAACTCCTTTCCATG   438
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   217 TGTCCACAGCCAGAGGGTCCTTTTGATTTTCCAAAAAACCCAGGGAACTCCCTTTCCATG   158

Qy   439 AGTACTCCAGGTCCTCCTTTGTGTAAGTAGCCTTTATCCCCAGCCTGAAATGTA   498
             |||||||||||||||||| ||| ||| |||||||||||||||||| ||||||||||
Db   157 AGCACTCTCAGGTCCTCCAGTTTGTCAAGTAGTTTTTTTCCCCTGCAAACCTGTGAAATGTA   98

Qy   499 AACATCATGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCCGTTGAA   558
             |||||||||||||||||||| || ||||||||| ||||||||||||||| |||||||||
Db   97 AGCATCATGTTTCCATGGCATGCTCCNATTTGGGATGGCATTTTGAAGAATCTGTTGAA   38

Qy   559 GCCTTGGCCGAGGCGCGGCGAGCGCTGGCGAG   591
             ||||| ||||| || ||||| ||||||| ||
Db   37 ACCTGGGCCCTGAGGCGCGCTGCAGTCTTTGGGAAG   5

RESULT 9
US-09-385-982-150
; Sequence 150, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(509)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-150

Query Match   13.7%; Score 164.8; DB 3; Length 509;
Best Local Similarity   70.9%; Pred. No. 1.9e-33;
Matches   195; Conservative   0; Mismatches   79; Indels   1; Gaps   1;

Qy   1 GGAACTAAAAAGAACTTTATTTATTGAGGCAAGGGGATGCAAACAATACAAAAATCAA   60
             ||||| ||||| |||||||||||||||||||| |||||||||||||||||||||||||
Db   5 GGAANNAAAAAAACTTTTTTTTTTNGGGGNNNGGGNTGCNANCNATNCAAAAATCAA   64

Qy   61 AAGCTTATCTGGTATTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT   120
             || ||| |||| ||||| || |||| ||||||||||||||||| ||||||||| ||
Db   65 AANCNTNTTGGGTTTAACTTTTTTTTTTTGNTTGNCAAANNAAAANTAAANTTTNTT   124

```
Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
          ||||| |||||||| ||| ||||| ||||||||||||| |||| ||||||||||||||||
Db    125 TTTANATTTGCTAANGGGCCNGANCNGCNNAAAAAAANCCTTTTTNGGGGAANCTTNGGG 184

Qy    181 GCAGATTCCTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCCGAACTGCTCATT 240
          ||||| ||| ||||||||||||||||||| |||| ||||||| ||| |||| ||||||||
Db    185 GCAAAATNNTNANCNACCCCTTGGGANAACTTTTNTTAGGGGGGNNNNAACCG-NCATT 243

Qy    241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTAC 275
          |||||| |||| ||| |||||||| ||||||| |
Db    244 TTTGCCCACTTTTTTCCCTTTGNTTAANGGGGNC 278
```

RESULT 10
US-09-680-420A-21/c
; Sequence 21, Application US/09680420A
; Patent No. 6528262
; GENERAL INFORMATION:
; APPLICANT: GILAD, Shlomit
; APPLICANT: EINAT, Paz
; APPLICANT: GROSMAN, Avital
; TITLE OF INVENTION: METHOD FOR ENRICHMENT OF NATURAL ANTISENSE MESSENGER RNA
; FILE REFERENCE: GILAD-2A
; CURRENT APPLICATION NUMBER: US/09/680,420A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/157,843
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Amplified Human
US-09-680-420A-21

Query Match   8.4%; Score 101; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 7.4e-17;
Matches   101; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy      1 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    157 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 98

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTTCTGCTTGTCAA 101
          ||||||||||||||||||||||||||||||||||||||||||||
Db     97 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTTCTGCTTGTCAA 57
```

RESULT 11
US-09-774-528-414/c
; Sequence 414, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y., Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 674361Ie1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802

; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 414
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (223)..(522)
US-09-774-528-414

Query Match   7.2%; Score 85.8; DB 4; Length 522;
Best Local Similarity 58.1%; Pred. No. 1.2e-12;
Matches   175; Conservative   0; Mismatches 117; Indels   9; Gaps   1;

```
Qy    253 TTTCCCTTCTGCTTCATGTGTACTACGTGTGCTACACAAAATAGTACAATGCAATGGTGAGGGCCCGCA 312
          ||||| |||||||| |||||| | ||||||||| |||||| || |||| ||| | ||| ||||| |||
Db    518 TTTCCTTTCTTCTTCAATTGTTCTACAAAGTAATCATTACAAGCAACTGTCCAGTCGTGCC 459

Qy    313 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACACTCGTCCAGGTCCTTC 372
          | |||| |||| ||| |||||||||||| ||  || || ||||||||||||||||||||
Db    458 ACCATGACCACGAATTCATTAAAATCCACTTCGTTGTCCTTATTGGCATCCAGGTCCTGC 399

Qy    373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAATCCAGGGAACTCCTTT 432
          |||||| |||| ||| |||| |||||||||||||| |||||||||| |||||||||||
Db    398 ACTATCTTATCAACCAACTGGGTTCCTTTTGGCACGAGAGGAATTCCGTGAGCTCTCGC 339

Qy    433 TCCATGAGTACTTCCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCC-------CCAGCG 483
          |||||| |||||| ||||||||| ||| || ||||||||  ||||          ||||||
Db    338 TGCAGGAGCAGTTTCAGTTCCCCCTTGCTGAGCTTGAATCTCTTCCTTGCCTTGCCAGAA 279

Qy    484 AATTTGTGAAATGTAAACATCATGGTTTCCATGGGCGTGTTCCATTTGAGATGGCATTTTG 543
          ||||| |||| |||||||||||||| |||||||||||||||| |||||||||||| ||
Db    278 TAGCGGTGGAAGATTCTAATCATGGTCCATGCATGGTGGGCATGTCG 219

Qy    544 G 544
          |
Db    218 G 218
```

RESULT 12
US-09-949-016-5370/c
; Sequence 5370, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5370
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5370

Query Match   6.3%; Score 75.2; DB 4; Length 592;
Best Local Similarity 61.0%; Pred. No. 7.8e-10;
Matches   122; Conservative   0; Mismatches   78; Indels   0; Gaps   0;

```
Qy    280 AAATAGTCATTGCATGCAATGCAATGTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCC 339
          || | |||| | ||| |||| |||||| |||||| | |||||||||||| |||  ||
```

```
Db    382 AAGAAATTGTTACAGGCCACTGTGAGAGCAGCCACAAGCACCACATACTCCTGGAAGTCC 323

Qy    340 ACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCT 399
              |||| |||||| || || ||||||||||||
Db    322 ACCTCCCGTCTCCATTCTCGTCTAGCTCCTTCATCACCTTGTCCACAGCATCCACATCC 263

Qy    400 TTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTT 459
              ||||| |||||| ||| ||  || ||||||||| ||||| |||
Db    262 TTCTGGGCATCCAGGAAGCCAGGAGAGCTCCGTCGCAGCAGCTCTTTCAGCTCCTTCTTG 203

Qy    460 GTTAAGTAGCCTTTATCCCC 479
              ||    ||| ||  ||
Db    202 CTCAGCTTGTACTTGTCCCC 183
```

RESULT 13
US-09-949-016-4686/c
; Sequence 4686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4686
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4686

Query Match   5.9%;   Score 71.2; DB 4; Length 434;
Best Local Similarity   61.2%; Pred. No. 7.7e-09;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
Qy    278 CAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGC 337
              ||||  ||| |  ||     |||  ||    |  |||  ||||| ||||||||||
Db    289 CAAAGTACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACTCACTGAAGT 230

Qy    338 CCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGT 397
              ||||  |||||||  || |||||||||| ||||  || ||||||  ||
Db    229 CCACCTGGGCATCTCCATTGGCGTCCAGGTCCTTGAGCAATTATCCACGGCATCCTTGT 170

Qy    398 CTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCT 457
              ||||| ||| || |||  || |||| |||||| ||||| |||||
Db    169 CTTTTCCACTCTGCGAGGAAGCCTGGTAGCTCCTTCTCCATCAGCACCTTGAGCTCCCCT 110

Qy    458 TTGTTAAG 465
              || |||
Db    109 TGGTCAGG 102
```

RESULT 14
US-09-814-915A-87/c
; Sequence 87, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; TITLE OF INVENTION: Thereto
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-87

Query Match   5.9%;   Score 71.2; DB 4; Length 439;
Best Local Similarity   61.2%; Pred. No. 7.7e-09;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
Qy    278 CAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGC 337
              ||||  ||| |  ||     |||  ||    |  |||  ||||| ||||||||||
Db    289 CAAAGTACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACTCACTGAAGT 230

Qy    338 CCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGT 397
              ||||  |||||||  || |||||||||| ||||  || ||||||  ||
Db    229 CCACCTGGGCATCTCCATTGGCGTCCAGGTCCTTGAGCAATTATCCACGGCATCCTTGT 170

Qy    398 CTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCT 457
              ||||| ||| || |||  || |||| |||||| ||||| |||||
Db    169 CTTTTCCACTCTGCGAGGAAGCCTGGTAGCTCCTTCTCCATCAGCACCTTGAGCTCCCCT 110

Qy    458 TTGTTAAG 465
              || |||
Db    109 TGGTCAGG 102
```

RESULT 15
US-09-919-172-101/c
; Sequence 101, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 101
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 1422432CB1
; NAME/KEY: unsure
; LOCATION: 205
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-101

Query Match   5.9%;   Score 71.2; DB 4; Length 860;
Best Local Similarity   61.2%; Pred. No. 1.1e-08;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
Qy    278 CAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGC 337
              ||||  ||| |  ||     |||  ||    |  |||  ||||| ||||||||||
Db    703 CAAAGTACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACTCACTGAAGT 644

Qy    338 CCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGT 397
              ||||  |||||||  || |||||||||| ||||  || ||||||  ||
Db    643 CCACCTGGGCATCTCCATTGGCGTCCAGGTCCTTGAGCAATTATCCACGGCATCCTTGT 584

Qy    398 CTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCT 457
              ||||| ||| || |||  || |||| |||||| ||||| |||||
Db    583 CTTTTCCACTCTGCGAGGAAGCCTGGTAGCTCCTTCTCCATCAGCACCTTGAGCTCCCCT 524
```

```
Qy  458 TTGTTAAG 465
        ||||||||
Db  523 TGGTCAGG 516


RESULT 16
US-09-976-594-466/c
; Sequence 466, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 466
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1422432CB1
; NAME/KEY: unsure
; LOCATION: 205
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-466

Query Match       5.9%;  Score 71.2;  DB 4;  Length 860;
Best Local Similarity  61.2%;  Pred. No. 1.1e-08;
Matches 115;  Conservative 0;  Mismatches 73;  Indels 0;  Gaps 0;

Qy  278 CAAAATAGTCATTGCATGCAATGGTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGC 337
        ||||| |||
Db  703 CAAAGTACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACTCACTGAAGT 644

Qy  338 CCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGT 397
        |||| ||| |||||| |||||| |||||||||
Db  643 CCACCTGGGCATCTCATTGGCGTCCAGGTCCTTGAGCAATTTATCCACGGCATCCTTGT 584

Qy  398 CTTTTTGATTTTCCAAAAATCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCT 457
        |||||  |||  ||||  |||||||||
Db  583 CTTTTCCACTCTGCAGGAAGCCTGGTAGCTCCTTCCATCAGCACCTTGAGCTCCCCCT 524

Qy  458 TTGTTAAG 465
        ||||||||
Db  523 TGGTCAGG 516


RESULT 17
US-09-513-999C-14895/c
; Sequence 14895, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Duclert, A.
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14895
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 53
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 54
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-14895

Query Match       5.8%;  Score 69;  DB 4;  Length 205;
Best Local Similarity  88.2%;  Pred. No. 2e-08;
Matches 75;  Conservative 0;  Mismatches 10;  Indels 0;  Gaps 0;

Qy  338 CCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGT 397
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  205 CCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGT 146

Qy  398 CTTTTTGATTTTCCAAAAATCCAGG 422
        |||||||| | |||
Db  145 CTTTTTGACCACGCTATGCTCCAAG 121


RESULT 18
US-09-566-921-119/c
; Sequence 119, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 119
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 021192.8
US-09-566-921-119

Query Match       5.4%;  Score 65.2;  DB 4;  Length 1081;
Best Local Similarity  55.2%;  Pred. No. 4.5e-07;
Matches 127;  Conservative 0;  Mismatches 103;  Indels 0;  Gaps 0;

Qy  250 TTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGCCC 309
        || |||  |||   |||| ||  |||||||||
Db  603 TTGGCTGCTTTCTAATCTCACTCATGTTCAAAGAACTCGTGCGGCAGGCAGTAGTAACCATG 544

Qy  310 GCAATTAGGGAAAGAAGCTCGGAGCCCACTTTGCCGAGCCCATCTCTACACTGGTCCAGTCC 369
        ||||| |||  |||  ||
Db  543 GCAACAAAGGCCATGAATTCCTGGAGTCACATTGTCCATCATTGTCCAGTGTT 484

Qy  370 TTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACTCC 429
        | |||  |||||||||  ||    |||||
Db  483 TCCATGACTTTGTCCACAACCTCCTGCTCTTTGATTTCCTCTAAGAAATGGGAAAGCTCA 424

Qy  430 TTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCC 479
        ||||
Db  423 TTGTTGATGAGCTCCTTCAGTTCGGATTTCTTCAGCTTGTGCTTGTCTCC 374


RESULT 19
US-09-919-039-183/c
; Sequence 183, Application US/09919039
; Patent No. 6727066
```

; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 183
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 2706645CB1
US-09-919-039-183

```
Query Match      5.3%;  Score 63.6;  DB 4;  Length 962;
Best Local Similarity  54.8%;  Pred. No. 1.1e-06;
Matches  126;  Conservative  0;  Mismatches 104;  Indels  0;  Gaps  0;

Qy   250 TTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGTGAGGCCC 309
          ||| | |||||    ||||| |  | ||||| |||| |||||  | || |||||||||
Db   557 TTGGCTGCTTTCTAATCTCACTCATGTTCAAAGAACTCGTGGCAGCAGTAGTAACCATG 498

Qy   310 GCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTCTACACTGTCCAGGTCC 369
          ||||  | |||    | |||| |  ||||||| | ||||||| |||||||
Db   497 GCAACAAAGGCCATGAATTCCTGGAAGTCACATTCGCCGTCTCCATTGTCCAGTGTT 438

Qy   370 TTCATTATTTTGTCCACAGCCAGAGAGGTCTTTTGATTTCCAAAAATCCAGGGAACTCC 429
          |||| |   | |||    |  ||||| ||| || | ||| ||||||| |||||  ||
Db   437 TCCATGACTTGTCCAACAACCTCCTGCTCTTTGATTTCCTGTAAGAAATGGGAAAGCTCA 378

Qy   430 TTTTCCATGAGTACTCTCAGGTCCTCCTTTGTAAGTAGCCTTTATCCCC 479
          | |   ||  | ||| ||| |  | | |||| ||| ||
Db   377 TTGTTGATGAGCTCCTTGAGTTCGGATTCTTCAGCTTGTGCTTGTCTCC 328
```

RESULT 20
US-09-513-999C-1413/c
; Sequence 1413, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; Patent No. 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1413
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..277
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 223
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 56
; OTHER INFORMATION: Xaa=Lys or Asn
US-09-513-999C-1413

```
Query Match      5.2%;  Score 62.2;  DB 4;  Length 279;
Best Local Similarity  66.2%;  Pred. No. 1.5e-06;
Matches  88;  Conservative  1;  Mismatches 44;  Indels  0;  Gaps  0;

Qy   333 GAAGCCACTTGCCATCTCTACACTGTCCAGGTCCTCATTATTTTGTCCAGCCAG 392
          ||||||||  |||||||  |||||||||||||||  | || ||||||||||||
Db   268 GAAGTCCACCTGGGCATCTCCATTGGCGTCCAGGTCCTTGAGCAAWTTATCCACGGCATC 209

Qy   393 AGGGTCTTTTTGATTTCCAAAAATCCAGGAACTCCTTTCCATGAGTAGTCTCAGTC 452
          ||||||  | |  ||  ||||||| ||||| ||| |||| | |||||  |||||
Db   208 CTTGTCTTTTCCACTCTGCAGGAGCCTGGTAGCTCCTCCTCTCCATCAGCACCTTGAGCTC 149

Qy   453 CTCCTTTGTTAAG 465
          | ||||| |||||
Db   148 CCCCTTGGTCAGG 136
```

RESULT 21
US-09-949-016-2162/c
; Sequence 2162, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2162
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2162

```
Query Match      4.5%;  Score 54.4;  DB 4;  Length 2592;
Best Local Similarity  51.0%;  Pred. No. 0.00047;
Matches  153;  Conservative  0;  Mismatches 146;  Indels  1;  Gaps  1;

Qy   538 ATTTTGTGTGTCCGTTGAAGCTTGCCGAGGCGGCGACGCTGGCGAGCTGGGC 597
          ||| ||| || || ||||||||||  ||||      ||||||||||||
Db   506 ATGTAGAGGGTGTCGCCCGAGGCCATGCTGAGGCGGCCGGCGCCGGCGGCGCC 447

Qy   598 GAGCTGGACGCGGGGGGCGGGAGGCGGAGCGGCGGGAGGAGGAGAGAGCCGGCAGG 657
          ||||          ||||       ||||   |||||    |  ||||||||||
Db   446 TCGGCTCCGGCTGACGAGGCGGCGGCGGGCGGCCGGCCGTGGGGAGGAAGGCA 387

Qy   658 GGCGGGTGGGTAGAGGAGGAGGCGCGCGGGAGGGAGGAGCCTCGGCAGG 717
          ||||     |||        |||||||||||||    |||||   ||
Db   386 GAGGGAGGAAGGCGGCGAGCGGGGGGGGGGGGGGAGAGGGGGCGGG 327

Qy   718 GCGCTCCCCCAGCCCTGTCTCCCCGGCGGCGGGGCTTCCCCGGC 777
          ||||||         | |||||| |||||| ||
Db   326 GCGCCGCGGCGGCGGGCGGGGCTTCCCGCTCCGGTGCCCCCGC 267

Qy   778 GCGC-GGCCCACGCCCTGCTCCGTCCGCTCTCCCGCTCCCGCGCCCC 836
          |||| |  | |||||||| | | |||| | ||| ||  |||||||
Db   266 TCGCTCGGCCGGCTGCGTCGTCTCCGCTCCCCGGCCAACCGCCCGC 207
```

RESULT 22
US-09-949-016-13904/c
; Sequence 13904, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 13904
; LENGTH: 43690
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13904

Query Match   4.5%;   Score 54.4; DB 4;   Length 43690;
Best Local Similarity   51.0%;   Pred. No. 0.0018;
Matches   153; Conservative   0; Mismatches 146; Indels   1; Gaps   1;

Qy   538 ATTTTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCCGCGGGCGGACGCTGGGGAGCTGGGC 597
               ||| ||| ||| |||||||| || || | ||| |||| ||||| |||||| ||||
Db   2506 ATGTAGAGGGTGTCGCCCGAGGCCATGGCTGAGGGCTCGAGGGCCCACGGCCCGCGCGGCC 2447

Qy   598 GAGCTGGACGCGGGGGGCGGAGAGGCGGAGAGGCGCGGGCGCGAGAGGCGGCGGCGGGCGG 657
               ||||| | |||||| | | ||| || ||||| |||| | ||||| || | ||||
Db   2446 TCGGCTCCTCCGCTCGGGGGCCGTGGGGCGGGCGGAGAGGCGGGCGGCCGCCCGTGGGACG 2387

Qy   658 GGCGGGTGGGTAGAGGAGGCGGCGGCGGCCGGCGGCGGGGAGGAGCCGTGGCCGGCTCCGG 717
               || ||| | | | ||| || || ||| || || | ||| || || ||||| ||||
Db   2386 GAGGAGGAAGGCGGCGAGCGGGCGAGCGGGGGCGGGCGGGGGAGGGGGCGGGGAAGGGGCG 2327

Qy   718 GCGCTCCCCAGCGCCCTGTCTCTCCTCTTCGCCCGGCCTCCCCGACCCCGGGC   777
               ||||| ||| ||| | |||| ||| || || | | ||||| ||||||
Db   2326 GCGCCCGCGGCGGGGGGGCGGCTTCCCGCGCTCCGGTGCGGCCCGCGCGCCGC 2267

Qy   778 GCGC-GGCCCACGCCCTGCCTCCCGCTCTCCCGGACCCGCCTCGCAGAGGCCTCGCCCGCCCC 836
               |||| | || ||||||| |||| | | |||| ||| || | || ||| ||||||||
Db   2266 TCGCTCGGCCCCGTGTCGTCTCGGCTCCTCCGGCTCCCCGCCCCTCCGCCGCCAACCGCCCGC 2207

RESULT 23
US-09-643-597-308/c
; Sequence 308, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-643-597-308

Query Match   4.5%;   Score 54.2; DB 3;   Length 421;
Best Local Similarity   51.1%;   Pred. No. 0.00023;
Matches   159; Conservative   0; Mismatches 143; Indels   9; Gaps   1;

Qy   238 ATTTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
               ||| | | || |||| || ||| || | | || |||| || || |||| ||||||
Db   352 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 293

Qy   298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
               |||| || || | || ||| | | ||| || ||||| || || |||||||| |
Db   292 ATGGCGATGCAGGACAGGAAGAACACAGTACTCTTGGAAGTCCACCTCGTTGTCCCTGTTG 233

Qy   358 TGGTCCAGTCTCTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAT 417
               ||| ||| | ||| | ||||| | ||| ||||| ||| | ||| || || ||
Db   232 CTGTCCAAGTTGCTCATCAGCTTCTGAAAGCAGCTTCATCTGTCCTTTTGTTAAGTAGCC 173

Qy   418 CCAGGGAACTCCTTTTCCGGGTCAGCAGTACTTCTCAGGTCCTCCTTTAGTTCTGAACTTGTTCATT 477
               ||||| | || | | ||||| || |||| | ||||| || |||| |||| ||||| || |
Db   172 CTGGGCAGCAGCTCCCGGGTCAGCAGTACTTGTGAAGGTGGACCACCATCACATCCAGGGCCTTCTCCAGA 113

Qy   478 --------CCAGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATT 528
                       ||||| || | | ||| | |||| | || ||| | ||| ||||| ||
Db   112 CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACCACCATCACATCCAGGGCCTTCTCCAGA 53

Qy   529 TGAGATGGCAT 539
               ||| | ||
Db   52 GGGCACGCCAT 42

RESULT 24
US-09-480-884A-308/c
; Sequence 308, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-480-884A-308

Query Match   4.5%;   Score 54.2; DB 4;   Length 421;
Best Local Similarity   51.1%;   Pred. No. 0.00023;
Matches   159; Conservative   0; Mismatches 143; Indels   9; Gaps   1;

Qy   238 ATTTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
               ||| | | || |||| || ||| || | | || |||| || || |||| ||||||
Db   352 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 293

Qy   298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
               |||| || || | || ||| | | ||| || ||||| || || |||||||| |
Db   292 ATGGCGATGCAGGACAGGAAGAACACAGTACTCTTGGAAGTCCACCTCGTTGTCCCTGTTG 233

Qy   358 TGGTCCAGTCTCTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAT 417
               ||| ||| | ||| | ||||| | ||| ||||| ||| | ||| || || ||
Db   232 CTGTCCAAGTTGCTCATCAGCTTCTGAAAGCAGCTTCATCTGTCCTTTTGTTAAGTAGCC 173

Qy   418 CCAGGGAACTCCTTTTCCGGGTCAGCAGTACTTCTCAGGTCCTCCTTTATCC 477
               ||||| | || | | ||||| || |||| | ||||| || |||| ||
Db   172 CTGGGCAGCAGCTCCCGGGTCAGCAGTACTTGTGAAGGTGGACCACCATCACATCCAGGGCCTTCTCCAGA 113

Left column

```
Qy   478  --------CCAGCGAATTGTGAAATGTAAACATCATGGTTCATGGCGTGTTCCATT  528
                  ||||||||||
Db   112  CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCCAGGGCCTTCTCCAGA  53

Qy   529  TGAGATGGCAT  539
                  |||||
Db    52  GGGCACGCCAT  42
```

RESULT 25
US-09-542-615A-308/c
; Sequence 308, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-542-615A-308

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Query Match       4.5%;     Score 54.2;   DB 4;   Length 421;
Best Local Similarity   51.1%;   Pred. No. 0.00023;
Matches 159;   Conservative   0;   Mismatches 143;   Indels   9;   Gaps   1;

Qy   238  ATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTCATGTGTACTACAAAATAGTCATTGCATGCA  297
          ||||||       |||||        |||||   || ||   |||||||||
Db   352  AGTTTTCATTTCTTCCTGGCCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC  293

Qy   298  ATGGTGAGGCCCGCAATTAGGAGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC  357
          ||||| |   |       |||||||||||   |||||||||
Db   292  ATGGCGATGCAGGACAGGAAGACACAGTACTTCTTGGAAGTCCACCTGTGTCCCTGTTG  233

Qy   358  TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAT  417
          ||||| |||| | ||| |       |||||||||
Db   232  CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGCAGCAGCTTCATCGTCCTTTTCCCCAAGAAG  173

Qy   418  CCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCC  477
          ||||| || |      |||||||  |||||||||
Db   172  CTGGGCAGCTCCCGGGTCAGCAGCTCCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA  113

Qy   478  --------CCAGCGAATTGTGAAATGTAAACATCATGGTTCATGGCGTGTTCCATT  528
                  ||||||||||
Db   112  CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCCAGGGCCTTCTCCAGA  53

Qy   529  TGAGATGGCAT  539
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Db    52  GGGCACGCCAT  42
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RESULT 26
US-09-606-421B-308/c
; Sequence 308, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.

Right column

; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-606-421B-308

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Query Match       4.5%;     Score 54.2;   DB 4;   Length 421;
Best Local Similarity   51.1%;   Pred. No. 0.00023;
Matches 159;   Conservative   0;   Mismatches 143;   Indels   9;   Gaps   1;

Qy   238  ATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTCATGTGTACTACAAAATAGTCATTGCATGCA  297
          ||||||       |||||        |||||   || ||   |||||||||
Db   352  AGTTTTCATTTCTTCCTGGCCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC  293

Qy   298  ATGGTGAGGCCCGCAATTAGGAGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC  357
          ||||| |   |       |||||||||||   |||||||||
Db   292  ATGGCGATGCAGGACAGGAAGACACAGTACTTCTTGGAAGTCCACCTGTGTCCCTGTTG  233

Qy   358  TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT  417
          ||||| |||| | ||| |       |||||||||
Db   232  CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGCAGCAGCTTCATCGTCCTTTTCCCCAAGAAG  173

Qy   418  CCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCC  477
          ||||| || |      |||||||  |||||||||
Db   172  CTGGGCAGCTCCCGGGTCAGCAGCTCCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA  113

Qy   478  --------CCAGCGAATTGTGAAATGTAAACATCATGGTTCATGGCGTGTTCCATT  528
                  ||||||||||
Db   112  CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCCAGGGCCTTCTCCAGA  53

Qy   529  TGAGATGGCAT  539
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Db    52  GGGCACGCCAT  42
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RESULT 27
US-09-630-940B-308/c
; Sequence 308, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-630-940B-308

Query Match   4.5%;   Score 54.2;   DB 4;   Length 421;
Best Local Similarity   51.1%;   Pred. No. 0.00023;
Matches 159;   Conservative   0;   Mismatches 143;   Indels   9;   Gaps   1;

Qy   238 ATTTCGCCTACTTCCTTCCCTTCCGTTCTCGCTTCATGTCATCATTACTGCTACTACAAAATAGTCATTGCATGCA 297
                                                       | | | ||||| | | | || || |||
Db   352 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGAAGCCCACTTGCCATCTCACAC 293

Qy   298 ATGGTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCACTTGCCATCTCACAC 357
                ||||| | | ||||||||||||||||| ||| ||
Db   292 ATGGGCGATGCAGCAGGAGCAGACACAGTAGTACTTGCCACCTCGTTGTCCCTGTTG 233

Qy   358 TGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
                |||| |||||| ||| ||| |||||||||||||||
Db   232 CTGTCCAAGTTGCTCATCAGCTTCTCGGAAAGCAGCTTCATCTGTCCTTTTCCCCAGAGAAG 173

Qy   418 CCAGGGAACTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCC 477
                || |||||||||||| ||| ||||||||||||||| ||||||| |||
Db   172 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA 113

Qy   478 --------CCAGCGAATTTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATT 528
                                    |||| || | || ||||||||||||||| ||||||
Db   112 CCCTCCTTTGCCCGAGTACTTGTGGGAAGGTGGACACCATCACACACCCAGGGGCCTTCTCCAGA 53

Qy   529 TGAGATGGCAT 539
                || ||||||
Db   52 GGGCACGCCAT 42

RESULT 28
US-09-370-838-281/c
; Sequence 281, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Raodoh
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;   TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;   FILE REFERENCE: 210121.475C1
;   CURRENT APPLICATION NUMBER: US/09/370,838
;   CURRENT FILING DATE: 1999-08-09
;   EARLIER APPLICATION NUMBER: US 09/285,323
;   EARLIER FILING DATE: 1999-04-02
;   NUMBER OF SEQ ID NOS: 289
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 281
;   LENGTH: 527
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (456)
;   OTHER INFORMATION: n=A,T,C or G
US-09-370-838-281

Query Match   4.5%;   Score 54.2;   DB 3;   Length 527;
Best Local Similarity   54.2%;   Pred. No. 0.00025;
Matches 110;   Conservative   0;   Mismatches 93;   Indels   0;   Gaps   0;

Qy   280 AAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCC 339
                || | ||||||| ||| |||| || ||||||||||||||||||| ||| |||
Db   316 AAGGAGTCATGCAAGCCATAGCTAGGCCACCAATCAGATTAAGAAATTCTGAGAAATCT 257

Qy   340 ACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCT 399
                |||||||| ||||| | ||| ||||||||| || |||| ||| ||| ||| |||
Db   256 AGCTGACCATCACTGTTGGTGTCCAGTTTCTTCATCATGCGGTCAAGGACACCAGGGTCC 197

Qy   400 TTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTTT 459
                ||||| |||||| | || |||| || | || || || | |||| |||
Db   196 TTCTGGTTCTTTGTGAAGGCAGCTAGTTCTGTATTCATGAGCTTAGGAACTCTCGTCTTG 137

Qy   460 GTTAAGTAGCCTTTATCCCCAGC 482
                ||||||||||||||||||||||||
Db   136 GAGAGAGTGTAGTTATAACCATC 114

RESULT 29
US-09-854-133-281/c
; Sequence 281, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
;   APPLICANT: Lodes, Michael J.
;   APPLICANT: Mohamath, Raodoh
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: Benson, Darin R.
;   APPLICANT: Secrist, Heather
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;   TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.475C10
;   CURRENT APPLICATION NUMBER: US/09/854,133
;   CURRENT FILING DATE: 2001-05-11
;   NUMBER OF SEQ ID NOS: 735
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 281
;   LENGTH: 527
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (456)
;   OTHER INFORMATION: n=A,T,C or G
US-09-854-133-281

Query Match   4.5%;   Score 54.2;   DB 4;   Length 527;
Best Local Similarity   54.2%;   Pred. No. 0.00025;
Matches 110;   Conservative   0;   Mismatches 93;   Indels   0;   Gaps   0;

Qy   280 AAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCC 339
                || | ||||||| ||| |||| || ||||||||||||||||||| ||| |||
Db   316 AAGGAGTCATGCAAGCCATAGCTAGGCCACCAATCAGATTAAGAAATTCTGAGAAATCT 257

Qy   340 ACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCT 399
                |||||||| ||||| | ||| ||||||||| || |||| ||| ||| ||| |||
Db   256 AGCTGACCATCACTGTTGGTGTCCAGTTTCTTCATCATGCGGTCAAGGACACCAGGGTCC 197

Qy   400 TTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTTT 459
                ||||| |||||| | || |||| || | || || || | |||| |||
Db   196 TTCTGGTTCTTTGTGAAGGCAGCTAGTTCTGTATTCATGAGCTTAGGAACTCTCGTCTTG 137

Qy   460 GTTAAGTAGCCTTTATCCCCAGC 482
                ||||||||||||||||||||||||
Db   136 GAGAGAGTGTAGTTATAACCATC 114

RESULT 30
US-08-190-560-3/c
; Sequence 3, Application US/08190560
; Patent No. 5798257
; GENERAL INFORMATION:
;   APPLICANT: Zain, Sayeeda
;   APPLICANT: Lukanidin, Eugene
;   TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
;   TITLE OF INVENTION: THE MTS-1 GENE
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
;   STREET: 400 Garden City Plaza
;   CITY: Garden City
;   STATE: New York
;   COUNTRY: United States
;   ZIP: 11530
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

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    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/190,560
    FILING DATE:
    CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
    NAME: DiGiglio, Frank S.
    REGISTRATION NUMBER: 31,346
    REFERENCE/DOCKET NUMBER: 7879ZY
    TELECOMMUNICATION INFORMATION:
    TELEPHONE: (516) 742-4343
    TELEFAX: (516) 742-4366
    TELEX: 230 901 SANS UR
    INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 579 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
    MOLECULE TYPE: cDNA
US-08-190-560-3

Query Match        4.5%;      Score 54.2;  DB 1;   Length 579;
Best Local Similarity  51.1%;  Pred. No. 0.00026;
Matches 159;  Conservative 0;  Mismatches 143;  Indels 9;  Gaps 1;

Qy  238 ATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
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Db  446 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 387

Qy  298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACAC 357
        |||| ||  || |
Db  386 ATGGCGATGCAGGACAGGAAGAAGACACAGTACTCTTGGAAGTCCACCTCGTTGTCCCTGTTG 327

Qy  358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
        || |||| |
Db  326 CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTTCCCCAAGAAG 267

Qy  418 CCAGGGAACTCCTTTCCATGAGTACTCTCAGTCCTCCTTGTTAAGTAGCCTTTATCC 477
        ||||| ||||
Db  266 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTAGTTCTGACTTGTTGAACTTGTCA 207

Qy  478 --------CCAGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATT 528
        |||  ||||
Db  206 CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCTCCAGA 147

Qy  529 TGAGATGGCAT 539
        |  ||
Db  146 GGGCACGCCAT 136

RESULT 31
US-08-469-277-3/c
; Sequence 3, Application US/08469277
; Patent No. 5801142
; GENERAL INFORMATION:
    APPLICANT: Zain, Sayeeda
    APPLICANT: Lukanidin, Eugene
    TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
    TITLE OF INVENTION: THE MTS-1 GENE
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
    STREET: 400 Garden City Plaza
    CITY: Garden City
    STATE: New York
    COUNTRY: United States
    ZIP: 11530
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
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    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/469,277
    FILING DATE:
    CLASSIFICATION:
    PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/190,560
    FILING DATE:
    ATTORNEY/AGENT INFORMATION:
    NAME: DiGiglio, Frank S.
    REGISTRATION NUMBER: 31,346
    REFERENCE/DOCKET NUMBER: 7879ZY
    TELECOMMUNICATION INFORMATION:
    TELEPHONE: (516) 742-4343
    TELEFAX: (516) 742-4366
    TELEX: 230 901 SANS UR
    INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 579 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
    MOLECULE TYPE: cDNA
US-08-469-277-3

Query Match        4.5%;      Score 54.2;  DB 1;   Length 579;
Best Local Similarity  51.1%;  Pred. No. 0.00026;
Matches 159;  Conservative 0;  Mismatches 143;  Indels 9;  Gaps 1;

Qy  238 ATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
        ||||| |  ||||||||||| | |||
Db  446 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 387

Qy  298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACAC 357
        |||| ||  || |
Db  386 ATGGCGATGCAGGACAGGAAGAAGACACAGTACTCTTGGAAGTCCACCTCGTTGTCCCTGTTG 327

Qy  358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
        || |||| |
Db  326 CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTTCCCCAAGAAG 267

Qy  418 CCAGGGAACTCCTTTCCATGAGTACTCTCAGTCCTCCTTGTTAAGTAGCCTTTATCC 477
        ||||| ||||
Db  266 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTAGTTCTGACTTGTTGAACTTGTCA 207

Qy  478 --------CCAGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATT 528
        |||  ||||
Db  206 CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCTCCAGA 147

Qy  529 TGAGATGGCAT 539
        |  ||
Db  146 GGGCACGCCAT 136

RESULT 32
US-08-468-946-3/c
; Sequence 3, Application US/08468946
; Patent No. 5843686
; GENERAL INFORMATION:
    APPLICANT: Zain, Sayeeda
    APPLICANT: Lukanidin, Eugene
    TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
    TITLE OF INVENTION: THE MTS-1 GENE
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
    STREET: 400 Garden City Plaza
    CITY: Garden City
    STATE: New York
    COUNTRY: United States
    ZIP: 11530
    COMPUTER READABLE FORM:
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        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/468,946
        FILING DATE: 06-JUN-1995
        CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/190,560
        FILING DATE: 31-JAN-1994
  ATTORNEY/AGENT INFORMATION:
        NAME: DiGiglio, Frank S.
        REGISTRATION NUMBER: 31,346
        REFERENCE/DOCKET NUMBER: 7879ZY
  TELECOMMUNICATION INFORMATION:
        TELEPHONE: (516) 742-4343
        TELEFAX: (516) 742-4366
        TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
        LENGTH: 579 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
  MOLECULE TYPE: cDNA
US-08-468-946-3

Query Match         4.5%;   Score 54.2;  DB 2;  Length 579;
Best Local Similarity 51.1%;  Pred. No. 0.00026;
Matches 159;  Conservative   0;  Mismatches 143;  Indels    9;  Gaps    1;

Qy  238 ATTTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
        ||||| ||| |||| || |||  ||| | ||  |||  |
Db  446 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 387

Qy  298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACAC 357
        ||||  ||| ||  |||||| || | |  ||||||
Db  386 ATGGCCATGCAGGACAGGAGACACAGTACTCTTGGAAGTCCACCTCGTTGTCCCTGTTG 327

Qy  358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
        ||||| |||| |  |||| || ||  |||| |  ||||
Db  326 CTGTCCAAGTTGCTCATCAGCTTCTCTCCTCCTTCCCCAGAG 267

Qy  418 CCAGGGAACTCCTTTTCCATGCAGTCTCCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCC 477
        ||| |  ||||||  ||  ||||||  ||||||
Db  266 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA 207

Qy  478 --------CCAGGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGCGGTGTTCCATT 528
                 ||||||| |  |||| ||||  |
Db  206 CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCTCCAGA 147

Qy  529 TGAGATGGCAT 539
        | | ||||||
Db  146 GGGCACGCCAT 136

RESULT 33
US-08-468-942-3/c
; Sequence 3, Application US/08468942
; Patent No. 5965360
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
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        ZIP: 11530
  COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/468,942
        FILING DATE: 06-JUN-1995
        CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/190,560
        FILING DATE: 31-JAN-1994
  ATTORNEY/AGENT INFORMATION:
        NAME: DiGiglio, Frank S.
        REGISTRATION NUMBER: 31,346
        REFERENCE/DOCKET NUMBER: 7879ZY
  TELECOMMUNICATION INFORMATION:
        TELEPHONE: (516) 742-4343
        TELEFAX: (516) 742-4366
        TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
        LENGTH: 579 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
  MOLECULE TYPE: cDNA
US-08-468-942-3

Query Match         4.5%;   Score 54.2;  DB 2;  Length 579;
Best Local Similarity 51.1%;  Pred. No. 0.00026;
Matches 159;  Conservative   0;  Mismatches 143;  Indels    9;  Gaps    1;

Qy  238 ATTTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
        ||||| ||| |||| || |||  ||| | ||  |||  |
Db  446 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 387

Qy  298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACAC 357
        ||||  ||| ||  |||||| || | |  ||||||
Db  386 ATGGCCATGCAGGACAGGAGACACAGTACTCTTGGAAGTCCACCTCGTTGTCCCTGTTG 327

Qy  358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
        ||||| |||| |  |||| || ||  |||| |  ||||
Db  326 CTGTCCAAGTTGCTCATCAGCTTCTCTCCTCCTTCCCCAGAG 267

Qy  418 CCAGGGAACTCCTTTTCCATGCAGTCTCCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCC 477
        ||| |  ||||||  ||  ||||||  ||||||
Db  266 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA 207

Qy  478 --------CCAGGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGCGGTGTTCCATT 528
                 ||||||| |  |||| ||||  |
Db  206 CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCTCCAGA 147

Qy  529 TGAGATGGCAT 539
        | | ||||||
Db  146 GGGCACGCCAT 136

RESULT 34
US-09-298-625-3/c
; Sequence 3, Application US/09298625
; Patent No. 6638504
; GENERAL INFORMATION:
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY THE MTS-1 GENE
; FILE REFERENCE: 7879ZYAIII-2
; CURRENT APPLICATION NUMBER: US/09/298,625
; CURRENT FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 08/468,942
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/190,560
; PRIOR FILING DATE: 1994-01-31
```

```
; PRIOR APPLICATION NUMBER: 07/981,455
; PRIOR FILING DATE: 1992-11-25
; PRIOR APPLICATION NUMBER: 07/550,600
; PRIOR FILING DATE: 1990-07-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-298-625-3

Query Match      4.5%;   Score 54.2;  DB 4;   Length 579;
Best Local Similarity   51.1%;   Pred. No. 0.00026;
Matches  159;  Conservative   0;   Mismatches 143;   Indels    9;   Gaps    1;

Qy   238 ATTTCTGCCTACTTCTTCCCTTCGCTTCGATTCATGTGTACTACAAAATAGTCATTGCATGCA 297
         |||| |  |||||||||
Db   446 AGTTTCATTTCTTCCTCTGGGCTGCTTATCTGGAAGCCTTCAAAGAATTCGTTACACATC 387

Qy   298 ATGGTGAGGCCCGCAATTAGGAGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACAC 357
         |||||||
Db   386 ATGGCGATGCAGGAAGACAGGAAGACAGTACTCTTGGAAGTCCACCTCGTTGTCCCTGTTG 327

Qy   358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
         |
Db   326 CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGAGCAGCTTCATCTGTCCTTTTCCCAAGAAG 267

Qy   418 CCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCC 477
         ||||| |||
Db   266 CTGGGCAGCTCCCGGGTCAGCAGTCTCCTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA 207

Qy   478 --------CCAGCGAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATT 528
                 |||| ||| |||
Db   206 CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCTCCAGA 147

Qy   529 TGAGATGGCAT 539
         |||||
Db   146 GGGCAGCCCAT 136


RESULT 35
US-09-949-016-14837
; Sequence 14837, Application US/0994916
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 14837
; LENGTH: 86380
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(86380)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14837

Query Match      4.5%;   Score 54;    DB 4;   Length 86380;
Best Local Similarity   52.2%;   Pred. No. 0.0031;
Matches  120;  Conservative   0;   Mismatches 110;   Indels    0;   Gaps    0;
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Qy   601 CTGGACGCGGGGGCGGGAGAGGCCGAGCGCGGCGGCGTGCGCCTTCCTTAGTAGTACGTGCGGC 660
         |||||| ||||||
Db  1651 CGGGACCCCGCCAGGAGGGGAGGGGCGCGGGGGGCGCGAACGAGCAGCCAAACAGTCGGAGC 1710

Qy   661 GGGTGGGTAGAGGAGGGCGCCGGGGAGGGAGGCGGCGGGAGCTCGGCGGCGCTCGGCAGGGCG 720
         || |||||||
Db  1711 GGAGAGATCGAAGGCTAGTGGCGGTGGGGGCGCAGCCGAGGCGTGGGAGGGGGTCC 1770

Qy   721 CTCCCCCAGCCTGTCTCCTCCCCCTTCCTGCCCCCGACTCCCCCGCCCCGGCGCCCCGG 780
         ||||| ||||
Db  1771 CGGCCGTCCTCGGCCCGCCCCTCCCCCGCCGCCCGCCCGCCCGCGGCGGGCCTCGGCAGGGGC 1830

Qy   781 CGGCCCACGCCCTGCCCTGCCTCCCGGACCCGCGCCGCTCCGCAGAGGCCTCGCC 830
         ||||| ||||
Db  1831 CCCGGCGCCCGCCCCCTGCCCGCGGCGGCGGCGCCGCGAGTCTCCTCCCC 1880


RESULT 36
US-08-190-560-1/c
; Sequence 1, Application US/08190560
; Patent No. 5798257
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,560
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 7872Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-190-560-1

Query Match      4.4%;   Score 53.2;  DB 1;   Length 303;
Best Local Similarity   51.3%;   Pred. No. 0.00036;
Matches  155;  Conservative   0;   Mismatches 138;   Indels    9;   Gaps    1;

Qy   247 TACTTCTTCCCTTCGCTTCGATTCATTGTACTACAAAATAGTCATTGCATGCAATGGTGAGG 306
         ||||||  ||||||
Db   302 TTCTTCCTGGGCTGCTTATCTGGAAGCCTTCAAAGAATTCGTTACATCATCATGGCGATG 243

Qy   307 CCCGCAATTAGGAGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGG 366
         ||||| |||||
Db   242 CAGGACAGGAAGACAGCACAGTACTCTTGGAAGTCCACCTCCACCTCGTTGTCGTTGCTCAAG 183
```

Qy　367　TCCTTCATTATTTTGTTCCACAGCCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGGGAAC　426
Db　182　TTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTTCCCCAGAAGAGCTGGGCAGC----　482
Qy　427　TCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC----　482
Db　122　TCCCGGGTCAGCAGCTCCTTTAGCTTGTGAGCTTGAACTTGTCACCCTCTTTG　63
Qy　483　----GAATTTGTGAAATGTAAACATCATGGTTCCATGCGTGTTCCATTTGAGATGGC　537
Db　62　CCCGAGTACTTGTGGAAGGTGACACCATCCAGGGCCTTCTCCAGAGGGCACGCC　3
Qy　538　AT　539
Db　2　AT　1

RESULT 37
US-08-469-277-1/c
; Sequence 1, Application US/08469277
; Patent No. 5801142
; GENERAL INFORMATION:
; - APPLICANT: Zain, Sayeeda
; - APPLICANT: Lukanidin, Eugene
; - TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; - TITLE OF INVENTION: THE MTS-1 GENE
; - NUMBER OF SEQUENCES: 9
; - CORRESPONDENCE ADDRESS:
; - ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; - STREET: 400 Garden City Plaza
; - CITY: Garden City
; - STATE: New York
; - COUNTRY: United States
; - ZIP: 11530
; - COMPUTER READABLE FORM:
; - MEDIUM TYPE: Floppy disk
; - COMPUTER: IBM PC compatible
; - OPERATING SYSTEM: PC-DOS/MS-DOS
; - SOFTWARE: PatentIn Release #1.0, Version #1.25
; - CURRENT APPLICATION DATA:
; - APPLICATION NUMBER: US/08/469,277
; - FILING DATE:
; - CLASSIFICATION:
; - PRIOR APPLICATION DATA:
; - APPLICATION NUMBER: US/08/190,560
; - FILING DATE:
; - ATTORNEY/AGENT INFORMATION:
; - NAME: DiGiglio, Frank S.
; - REGISTRATION NUMBER: 31,346
; - REFERENCE/DOCKET NUMBER: 7879ZY
; - TELECOMMUNICATION INFORMATION:
; - TELEPHONE: (516) 742-4343
; - TELEFAX: (516) 742-4366
; - TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; - SEQUENCE CHARACTERISTICS:
; - LENGTH: 303 base pairs
; - TYPE: nucleic acid
; - STRANDEDNESS: double
; - TOPOLOGY: linear
; - MOLECULE TYPE: cDNA
US-08-469-277-1

Query Match　　　4.4%;　　Score 53.2;　DB 1;　Length 303;
Best Local Similarity　51.3%;　Pred. No. 0.00036;
Matches　155;　Conservative　0;　Mismatches 138;　Indels　9;　Gaps　1;

Qy　247　TACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGG　306
Db　302　TTCTTCCTGGGCTGCTTATCTGGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGG　243
Qy　307　CCCGCAATTAGGAGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGG　366

Db　242　CAGGACAGGAAGACACAGTACTCTTGGAAGTCCACCTCGTTGTCCCGTTGCTGTGTCCAAG　183
Qy　367　TCCTTCATTATTTTGTTCCACCGCCAGAGGGGTCTTTTTGATTTTCCAAAAATCCAGGGAAC　426
Db　182　TTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTTCCCCAGAAGAGCTGGGCAGC　123
Qy　427　TCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC---　482
Db　122　TCCCGGGTCAGCAGCTCCTTTAGCTTGTGAGCTTGAACTTGTCACCCTCTTTG　63
Qy　483　----GAATTTGTGAAATGTAAACATCATGGTTCCATGCGTGTTCCATTTGAGATGGC　537
Db　62　CCCGAGTACTTGTGGAAGGTGACACCATCCAGGGCCTTCTCCAGAGGGCACGCC　3
Qy　538　AT　539
Db　2　AT　1

RESULT 38
US-08-468-946-1/c
; Sequence 1, Application US/08468946
; Patent No. 5843686
; GENERAL INFORMATION:
; - APPLICANT: Zain, Sayeeda
; - APPLICANT: Lukanidin, Eugene
; - TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; - TITLE OF INVENTION: THE MTS-1 GENE
; - NUMBER OF SEQUENCES: 9
; - CORRESPONDENCE ADDRESS:
; - ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; - STREET: 400 Garden City Plaza
; - CITY: Garden City
; - STATE: New York
; - COUNTRY: United States
; - ZIP: 11530
; - COMPUTER READABLE FORM:
; - MEDIUM TYPE: Floppy disk
; - COMPUTER: IBM PC compatible
; - OPERATING SYSTEM: PC-DOS/MS-DOS
; - SOFTWARE: PatentIn Release #1.0, Version #1.25
; - CURRENT APPLICATION DATA:
; - APPLICATION NUMBER: US/08/468,946
; - FILING DATE: 06-JUN-1995
; - CLASSIFICATION: 435
; - PRIOR APPLICATION DATA:
; - APPLICATION NUMBER: US 08/190,560
; - FILING DATE: 31-JAN-1994
; - ATTORNEY/AGENT INFORMATION:
; - NAME: DiGiglio, Frank S.
; - REGISTRATION NUMBER: 31,346
; - REFERENCE/DOCKET NUMBER: 7879ZY
; - TELECOMMUNICATION INFORMATION:
; - TELEPHONE: (516) 742-4343
; - TELEFAX: (516) 742-4366
; - TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; - SEQUENCE CHARACTERISTICS:
; - LENGTH: 303 base pairs
; - TYPE: nucleic acid
; - STRANDEDNESS: double
; - TOPOLOGY: linear
; - MOLECULE TYPE: cDNA
US-08-468-946-1

Query Match　　　4.4%;　　Score 53.2;　DB 2;　Length 303;
Best Local Similarity　51.3%;　Pred. No. 0.00036;
Matches　155;　Conservative　0;　Mismatches 138;　Indels　9;　Gaps　1;

Qy　247　TACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGG　306
Db　302　TTCTTCCTGGGCTGCTTATCTGGGAAGCCCTCAAAGAATTCGTTACACATCGGTCCATG　243

Qy   307 CCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGG 366
          |||| ||||| ||||||| ||||||||||| |||||||||
Db   302 TTCTTCCTGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATCATGCGGATG 243

Qy   242 CAGGACAGGAAGAAGCACAGTACTCTTGGAAGTCCACCTGTGTCCCTGTTGCTGTCCAAG 183
          |||||| ||||||| ||||| ||||||||||
Db   307 CCCGCAATTAGGGAAAGAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGG 366

Qy   367 TCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAAC 426
          |||| |||| |||| |||||||| |||||||| | |||||||||
Db   242 CAGGACAGGAAGACACAGTACTCTTGGAAGTCCACCTGTGTCCCTGTTGCTGTCCAAG 183

Qy   182 TTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTCCCCAAGAAGCTGGGCAGC 123
          ||||| |||||||| | |||||||||||||||| |||||||||||||||
Db   367 TCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAAC 426

Qy   427 TCCTTTTCCATGAGTAGTCTCAGTCCTCCTTGTTAAGTAGCTTTATCCCCAGC---- 482
          |||||| ||||||||||||| ||||| |||||||||||||||||
Db   182 TTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTCCCCAAGAAGCTGGGCAGC 123

Qy   122 TCCCGGGTCAGCAGCTCCTTAGCTCTGACTTGTTGAGCTTGAACTTGTCACCCTCTTTG 63
          ||||||| | |||||||||||||||||||| ||||||||||||||||
Db   427 TCCTTTTCCATGAGTAGTCTCAGTCCTCCTTGTTAAGTAGCTTTATCCCCAGC---- 482

Qy   483 -----GAATTGTGAAATGTAAACATCAGTGGTTCCATGGCGTGTTCCATTTGAGATGGC 537
          ||||| | ||||||||||||
Db   122 TCCCGGGTCAGCAGCTCCTTAGCTCTGACTTGTTGAGCTTGAACTTGTCACCCTCTTTG 63

Qy   538 AT 539
          ||
Db   2 AT 1

RESULT 39
US-08-468-942-1/c
; Sequence 1, Application US/08468942
; Patent No. 5965360
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
;   STREET: 400 Garden City Plaza
;   CITY: Garden City
;   STATE: New York
;   COUNTRY: United States
;   ZIP: 11530
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/468,942
;   FILING DATE: 06-JUN-1995
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/190,560
;   FILING DATE: 31-JAN-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: DiGiglio, Frank S.
;   REGISTRATION NUMBER: 31,346
;   REFERENCE/DOCKET NUMBER: 7879ZY
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (516) 742-4343
;   TELEFAX: (516) 742-4366
;   TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 303 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-468-942-1

Query Match   4.4%;   Score 53.2; DB 2;   Length 303;
Best Local Similarity   51.3%;   Pred. No. 0.00036;
Matches 155;   Conservative   0;   Mismatches 138;   Indels   9;   Gaps   1;

Qy   247 TACTTCTTCCCTCTGCTTCCCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGG 306
          |||| ||| || | ||| | |||| ||||| | |||||||| |||| ||||| || ||

; ----------------------

Db   302 TTCTTCCTGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATCATGCGGATG 243

Qy   307 CCCGCAATTAGGGAAAGAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAAG 183

Db   242 CAGGACAGGAAGACACAGTACTCTTGGAAGTCCACCTGTGTCCCTGTTGCTGTCCAAG 183

Qy   367 TCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAAC 426

Db   182 TTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTCCCCAAGAAGCTGGGCAGC 123

Qy   427 TCCTTTTCCATGAGTAGTCTCAGTCCTCCTTGTTAAGTAGCTTTATCCCCAGC---- 482

Db   122 TCCCGGGTCAGCAGCTCCTTAGCTCTGACTTGTTGAGCTTGAACTTGTCACCCTCTTTG 63

Qy   483 -----GAATTGTGAAATGTAAACATCAGTGGTGGACCACCATCACATCCCAGGGCCCTTCTCCAGAGGGCACGCC 3

Db   62 CCCGAGTACTTGTGGAAGGTGGACCACCATCACATCCCAGGGCCCTTCTCCAGAGGGCACGCC 3

Qy   538 AT 539
          ||
Db   2 AT 1

RESULT 40
US-09-298-625-1/c
; Sequence 1, Application US/0929825
; Patent No. 6638504
; GENERAL INFORMATION:
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY THE MTS-1 GENE
; FILE REFERENCE: 7879ZYAIII-Z
; CURRENT APPLICATION NUMBER: US/09/298,625
; CURRENT FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 08/468,942
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/190,560
; PRIOR FILING DATE: 1994-01-31
; PRIOR APPLICATION NUMBER: 07/981,455
; PRIOR FILING DATE: 1992-11-25
; PRIOR APPLICATION NUMBER: 07/550,600
; PRIOR FILING DATE: 1990-07-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-298-625-1

Query Match   4.4%;   Score 53.2; DB 4;   Length 303;
Best Local Similarity   51.3%;   Pred. No. 0.00036;
Matches 155;   Conservative   0;   Mismatches 138;   Indels   9;   Gaps   1;

Qy   247 TACTTCTTCCCTCTGCTTCCCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGG 306

Db   302 TTCTTCCTGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATCATGCGGATG 243

Qy   307 CCCGCAATTAGGGAAAGAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAAG 183

Db   242 CAGGACAGGAAGACACAGTACTCTTGGAAGTCCACCTGTGTCCCTGTTGCTGTCCAAG 183

Qy   367 TCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAAC 426

Db   182 TTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTCCCCAAGAAGCTGGGCAGC 123

Qy   427 TCCTTTTCCATGAGTAGTCTCAGTCCTCCTTGTTAAGTAGCTTTATCCCCAGC---- 482

Db   122 TCCCGGGTCAGCAGCTCCTTAGCTCTGACTTGTTGAGCTTGAACTTGTCACCCTCTTTG 63

Qy   483 -----GAATTGTGAAATGTAAACATCAGTGGTGGACCACCATCACATCCCAGGGCCCTTCTCCAGAGGGCACGCC 3

Db   62 CCCGAGTACTTGTGGAAGGTGGACCACCATCACATCCCAGGGCCCTTCTCCAGAGGGCACGCC 3

Qy 538 AT 539
         ||
Db   2 AT 1

RESULT 41
US-07-662-198B-1/c
; Sequence 1, Application US/07662198B
; Patent No. 5262528
; GENERAL INFORMATION:
;   APPLICANT: Sager, Ruth
;   APPLICANT: Lee, Sam W.
;   APPLICANT: Tomasetto, Catherine
;   TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: U.S.A.
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   COMPUTER: IBM PS/2 Model 50Z or 55SX
;   OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
;   SOFTWARE: WordPerfect (Version 5.0)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/662,198B
;   FILING DATE: 19910228
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Fraser, Janis K.
;   REGISTRATION NUMBER: 34,819
;   REFERENCE/DOCKET NUMBER: 00530/049001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 542-5070
;   TELEFAX: (617) 542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 452
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-07-662-198B-1

Query Match   4.4%; Score 52.8; DB 1; Length 452;
Best Local Similarity   54.0%; Pred. No. 0.00055;
Matches 108; Conservative   0; Mismatches 92; Indels   0; Gaps   0;

Qy 280 AAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCC 339
Db 316 AAGAAGTCATTGCACATGACAGTGATGAGTGCCAGGAAAAACAGCATACTCCTGGAAGTCC 257

Qy 340 ACTTTGCCATCTCTACACTGGTTCTCATCCAGGTTGCCCATCCAGCGCCTTCAGCGGGTCT 399
Db 256 ACCTGCTGGTCACTGTTCTCATCCAGGTTGCCCATCCAGCTTCTTCAGCCCCTCCTCATCC 197

Qy 400 TTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCCTCAGGTCCTCCTTT 459
Db 196 ACTTTCTCCCCCACAAAGCTGGGCAGCTCCTTGTGCAGAAGTTCCTTCATTTCCCCCTTA 137

Qy 460 GTTAAGTAGCCTTTATCCCC 479
Db 136 CTCAGCTTGAACTTGTCGCC 117

RESULT 42
US-08-322-742-1/c

; Sequence 1, Application US/08322742
; Patent No. 5688641
; GENERAL INFORMATION:
;   APPLICANT: Sager, Ruth
;   TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: U.S.A.
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   COMPUTER: IBM PS/2 Model 50Z or 55SX
;   OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
;   SOFTWARE: WordPerfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/322,742
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/938,823
;   FILING DATE: September 1, 1992
;   APPLICATION NUMBER: 07/844,296
;   FILING DATE: February 28, 1992
;   APPLICATION NUMBER: 07/552,216
;   FILING DATE: February 28, 1991
;   ATTORNEY/AGENT INFORMATION:.
;   NAME: Fraser, Janis K.
;   REGISTRATION NUMBER: 34,819
;   REFERENCE/DOCKET NUMBER: 00530/048003
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 542-5070
;   TELEFAX: (617) 542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 452
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-322-742-1

Query Match   4.4%; Score 52.8; DB 1; Length 452;
Best Local Similarity   54.0%; Pred. No. 0.00055;
Matches 108; Conservative   0; Mismatches 92; Indels   0; Gaps   0;

Qy 280 AAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCC 339
Db 316 AAGAAGTCATTGCACATGACAGTGATGAGTGCCAGGAAAAACAGCATACTCCTGGAAGTCC 257

Qy 340 ACTTTGCCATCTCTACACTGGTTCTCATCCAGGTTGCCCATCCAGCGCCTTCAGCGGGTCT 399
Db 256 ACCTGCTGGTCACTGTTCTCATCCAGGTTGCCCATCCAGCTTCTTCAGCCCCTCCTCATCC 197

Qy 400 TTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCCTCAGGTCCTCCTTT 459
Db 196 ACTTTCTCCCCCACAAAGCTGGGCAGCTCCTTGTGCAGAAGTTCCTTCATTTCCCCCTTA 137

Qy 460 GTTAAGTAGCCTTTATCCCC 479
Db 136 CTCAGCTTGAACTTGTCGCC 117

RESULT 43
US-09-702-705-1585/c
; Sequence 1585, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Lodes, Michael A.

```
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C14
;  CURRENT APPLICATION NUMBER: US/09/702,705
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  1833
;  SOFTWARE:  FastSEQ for Windows Version 3.0
;  SEQ ID NO 1585
;    LENGTH: 392
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-702-705-1585

Query Match             4.4%;    Score 52.6;  DB 4;   Length 392;
Best Local Similarity  50.8%;    Pred. No. 0.00058;
   Matches  158;     Conservative   0;  Mismatches  144;  Indels   9;  Gaps   1;

Qy    238 ATTTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
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Db    364 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 305

Qy    298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
          ||||| || ||| ||||||||| || || ||||| ||||| ||||||||||  ||| ||
Db    304 ATGGCGATGCAGGACAGGAAGACACAGTACTCTTAGAAGTCCACCTCGTTGTCCCTGTTG 245

Qy    358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
          |||||| ||| ||||| | ||  || ||||| ||||| ||||| ||||| |||| || ||
Db    244 CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTTCCCCAAGAAG 185

Qy    418 CCAGGGAACTCCTTTCCTTGCTTCATGAGTACTCCAGTCCTCCTTGTTGTTAAGTAGCCTTTATCC 477
          ||||| || |  ||  |||||| || ||  |  |||| ||||  ||| | |||
Db    184 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA 125

Qy    478 CCAGC--------GAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATT 528
          ||||        |||||| ||||| |||| ||| |||||| ||||| ||||  ||||
Db    124 CCCTCTTTGCCCGAGTACTTGTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCCAGA 65

Qy    529 TGAGATGGCAT 539
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Db     64 GGGCACGCCAT 54


RESULT 45
US-09-614-124B-1585/c
;  Sequence 1585, Application US/09614124B
;  Patent No. 6630574
;  GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C9
;  CURRENT APPLICATION NUMBER: US/09/614,124B
;  CURRENT FILING DATE:  2001-07-11
;  NUMBER OF SEQ ID NOS:  1668
;  SOFTWARE:  FastSEQ for Windows Version 3.0
;  SEQ ID NO 1585
;    LENGTH: 392
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-614-124B-1585

Query Match             4.4%;    Score 52.6;  DB 4;   Length 392;
Best Local Similarity  50.8%;    Pred. No. 0.00058;
   Matches  158;     Conservative   0;  Mismatches  144;  Indels   9;  Gaps   1;

Qy    238 ATTTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
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Db    364 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 305

Qy    298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
          ||||| || ||| ||||||||| || || ||||| ||||| ||||||||||  ||| ||
Db    304 ATGGCGATGCAGGACAGGAAGACACAGTACTCTTAGAAGTCCACCTCGTTGTCCCTGTTG 245

Qy    358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAT 417
          |||||| ||| ||||| | ||  || ||||| ||||| ||||| ||||| |||| || ||
Db    244 CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTTCCCCAAGAAG 185
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; ORGANISM: Homo sapiens
US-09-736-457-1585

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Query Match             4.4%;    Score 52.6;  DB 4;   Length 392;
Best Local Similarity  50.8%;    Pred. No. 0.00058;
   Matches  158;     Conservative   0;  Mismatches  144;  Indels   9;  Gaps   1;

Qy    238 ATTTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCA 297
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Db    364 AGTTTTCATTTCTTCCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACACATC 305

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Db    244 CTGTCCAAGTTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCCTTTTCCCCAAGAAG 185

Qy    418 CCAGGGAACTCCTTTCCTTGCTTCATGAGTACTCCAGTCCTCCTTGTTGTTAAGTAGCCTTTATCC 477
          ||||| || |  ||  |||||| || ||  |  |||| ||||  ||| | |||
Db    184 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA 125

Qy    478 CCAGC--------GAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATT 528
          ||||        |||||| ||||| |||| ||| |||||| ||||| ||||  ||||
Db    124 CCCTCTTTGCCCGAGTACTTGTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCCAGA 65

Qy    529 TGAGATGGCAT 539
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Db     64 GGGCACGCCAT 54


RESULT 44
US-09-736-457-1585/c
;  Sequence 1585, Application US/09736457
;  Patent No. 6509448
;  GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
;  SEQ ID NO 1585
;    LENGTH: 392
;    TYPE: DNA
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Qy   418 CCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCC 477
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Db   184 CTGGGCAGCTCCCGGGTCAGCAGCTCCTTTAGTTCTGACTTGTTGAGCTTGAACTTGTCA 125

Qy   478 CCAGC-------GAATTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATT 528
             || |        | ||||||| || ||| |||| |||| |||| |||| ||||
Db   124 CCCTCTTTGCCCGAGTACTTGTGGAAGGTGGACACCATCACATCCAGGGCCTTCTCCAGA 65

Qy   529 TGAGATGGCAT 539
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Db    64 GGGCACGCCAT 54
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Search completed: August 17, 2005, 22:33:07
Job time : 247 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      August 17, 2005, 22:20:57 ; Search time 793 Seconds
                                 (without alignments)
                       9823.210 Million cell updates/sec

Title:         US-10-735-577-16
Perfect score: 1199
Sequence:      1 ggaactaaaaagaactta.........cgggcttccgcgcccaccgg 1199

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters:     14632570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications NA:*
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       2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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       5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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      20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
      21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
      22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
      23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
      24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
      25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	1199	100.0	1199	19	US-10-735-577-16	Sequence 16, Appl
c 2	1199	100.0	1199	19	US-10-735-577-17	Sequence 17, Appli
c 3	703.4	58.7	1124	13	US-10-044-090-1	Sequence 1, Appli
c 4	634	52.9	1893	9	US-09-925-301-586	Sequence 586, App
c 5	634	52.9	1893	10	US-09-997-003-13	Sequence 13, Appl
c 6	601	50.1	649	9	US-09-880-107-2350	Sequence 2350, Ap
c 7	601	50.1	649	17	US-10-172-118-847	Sequence 847, App
c 8	601	50.1	649	18	US-10-342-887-847	Sequence 847, Appl
c 9	601	50.1	649	20	US-10-487-337-7	Sequence 7, Appli
c 10	601	50.1	649	21	US-10-956-157-979	Sequence 979, App
c 11	601	50.1	649	21	US-10-956-157-6214	Sequence 6214, Ap
c 12	595.8	49.7	663	17	US-10-264-049-1114	Sequence 1114, Ap
c 13	577.4	48.2	608	13	US-10-027-632-261591	Sequence 261591,
c 14	577.4	48.2	608	17	US-10-027-632-261591	Sequence 261591,
c 15	537	44.8	571	9	US-09-920-300A-890	Sequence 890, App
c 16	537	44.8	571	13	US-10-033-528-890	Sequence 890, App
c 17	537	44.8	571	16	US-10-099-926-890	Sequence 890, App
c 18	537	44.8	571	22	US-10-961-527-890	Sequence 890, App
c 19	516	43.0	538	17	US-10-242-535A-47618	Sequence 47618, A
c 20	516	43.0	538	18	US-10-085-783A-47618	Sequence 47618, A
c 21	485.2	40.5	2016	10	US-09-992-600A-1	Sequence 1, Appli
c 22	485.2	40.5	2016	10	US-09-924-340-1	Sequence 1, Appli
c 23	485.2	40.5	2016	10	US-09-992-095B-1	Sequence 1, Appli
c 24	485.2	40.5	2016	14	US-09-999-570-1	Sequence 1, Appli
c 25	485.2	40.5	2016	14	US-10-000-489-1	Sequence 1, Appli
c 26	485.2	40.5	2016	14	US-10-000-986-1	Sequence 1, Appli
c 27	485.2	40.5	2016	16	US-10-154-678-1	Sequence 1, Appli
c 28	485.2	40.5	2016	16	US-10-001-142-1	Sequence 1, Appli
c 29	485.2	40.5	2016	21	US-10-838-854-1	Sequence 1, Appli
c 30	471.6	39.3	482	17	US-10-242-535A-46392	Sequence 46392, A
c 31	471.6	39.3	482	18	US-10-085-783A-46392	Sequence 46392, A
c 32	461.4	38.5	472	17	US-10-242-535A-57930	Sequence 57930, A
c 33	461.4	38.5	472	18	US-10-085-783A-57930	Sequence 57930, A
c 34	448	37.4	480	17	US-10-242-535A-49122	Sequence 49122, A
c 35	448	37.4	480	18	US-10-085-783A-49122	Sequence 49122, A
c 36	446.4	37.2	474	17	US-10-242-535A-56036	Sequence 56036, A
c 37	446.4	37.2	474	18	US-10-085-783A-56036	Sequence 56036, A
c 38	434.4	36.2	448	17	US-10-242-535A-56504	Sequence 56504, A
c 39	434.4	36.2	448	18	US-10-085-783A-56504	Sequence 56504, A
c 40	429.4	35.8	477	10	US-09-918-995-21508	Sequence 21508, A
c 41	422	35.2	466	10	US-09-918-995-12556	Sequence 12556, A
c 42	411	34.3	441	10	US-09-997-003-26	Sequence 26, Appl
c 43	396.2	33.0	632	15	US-10-106-698-2418	Sequence 2418, Ap
c 44	377.4	31.5	392	17	US-10-242-535A-45565	Sequence 45565, A
c 45	377.4	31.5	392	18	US-10-085-783A-45565	Sequence 45565, A

ALIGNMENTS

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RESULT 1
US-10-735-577-16
; Sequence 16, Application US/1073,577
; Publication No. US2004014289 7A1
; GENERAL INFORMATION:
;  APPLICANT: Waisman, David M.
;  TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastas
;  FILE REFERENCE: ME03-009
;  CURRENT APPLICATION NUMBER: US/10/735,577
;  CURRENT FILING DATE: 2003-12-12
;  PRIOR APPLICATION NUMBER: US 60/433,140
;  PRIOR FILING DATE: 2002-12-13
;  NUMBER OF SEQ ID NOS: 160
;  SOFTWARE: Microsoft Word
; SEQ ID NO 16
;  LENGTH: 1199
;  TYPE: DNA
;  ORGANISM: mammalian
US-10-735-577-16

Query Match             100.0%;  Score 1199;  DB 19;  Length 1199;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1199;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 GGAACTAAAAAGAACTTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db          1 GGAACTAAAAAGAACTTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60

Qy         61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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RESULT 2
US-10-735-577-17/c
; Sequence 17, Application US/10735577
; Publication No. US20040142897A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastas;
; FILE REFERENCE: ME03-009
; CURRENT APPLICATION NUMBER: US/10/735,577
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/433,140
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word
; SEQ ID NO 17
;   LENGTH: 1199
;   TYPE: DNA
;   ORGANISM: mammalian
US-10-735-577-17

Query Match   100.0%; Score 1199; DB 19; Length 1199;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1199; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1199 GGAACTAAAAAAAGAACTTATTTATTGAGGGATGCAAGGGGGATGCAAACAATACAAAAATCAA 1140

Qy   61 AAGCTTATCTGTATTTAACTTTTCTTCTCGCTGTCAAATGAGAGTTAGATTTTATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 AAGCTTATCTGTATTTAACTTTTCTTCTCGCTGTCAAATGAGAGTTAGATTTTATT 1080

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGTCATGCAATG 180
              |||||||||||||||||||||||||||||||||||||||||||
Db   1079 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGTCATGCAATG 1020

Qy   181 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 960

Qy   241 TCTGCCTACTTCTTTCCCTTCTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   959 TCTGCCTACTTCTTTCCCTTCTCATGTGTACTACAAAATAGTCATTGCATGCAATG 900

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   899 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 840

Qy   361 TCCAGTCCTTCATTATTTTCCATGCCTTTAAGTAGCCTTTATCCCCA 420
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Qy   421 GGGAACTCCTTTTCCATGAGTACTCTCAGTCCTCCGGTTAAGTGGTTCCATTGAGATGCATT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   779 GGGAACTCCTTTTCCATGAGTACTCTCAGTCCTCCGGTTAAGTGGTTCCATTGAGATGCATT 720

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Db   719 GCGAATTTGTGTAAACATCATCATGGTTCCATTTGAGATGCATT 660

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Db   659 TTGGTGTGGTCCGTTGAAGCCTTGCGAGCGCGGAGGCGGAGCGCGGGGCGCGGAG 600

Qy   601 CTGGACGCGGGGCGGAGAGGCCGGAGGCGGCGGCGGCGGCTGTGCGCCTTCCTTAGTACGTGCGGC 660
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Db   599 CTGGACGCGGGGCGGAGAGGCCGGAGGCGGCGGCGGCGGCTGTGCGCCTTCCTTAGTACGTGCGGC 540

Qy   661 GGGTGGTAGAGGAGGGGCGGCGGGAGCGCGGGGCGCGGGGCGCGGGGCG 720
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Db   539 GGGTGGTAGAGGAGGGGCGGCGGGAGCGCGGGGCGCGGGGCGCGGGGCG 480

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Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGTCATGCAATG 180

Qy   181 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240

Qy   241 TCTGCCTACTTCTTTCCCTTCTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300

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Qy   361 TCCAGTCCTTCATTATTTTCCATGCCTTTAAGTAGCCTTTATCCCCA 420

Qy   421 GGGAACTCCTTTTCCATGAGTACTCTCAGTCCTCCGGTTAAGTGGTTCCATTGAGATGCATT 480

Qy   481 GCGAATTTGTGTAAACATCATCATGGTTGTTCCATTGTCATTTCCATTGAGATGGCATT 540

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGCGAGCGCGGAGGCGGAGCTGGGCGGAG 600

Qy   601 CTGGACGCGGGGCGGAGAGGCCGGAGGCGGCGGCGGCGGCTGTGCGCCTTCCTTAGTACGTGCGGC 660

Qy   661 GGGTGGTAGAGGAGGGGCGGCGGGAGCGCGGGGCGCGGGGCGCGGGGCG 720

Qy   721 CTCCCCAGCCGTCTCTTCCCCTCCCCGACTCCCCGACCCCGGGCGCG 780

Qy   781 CGGCCCACGCGCCCTGCCCTCGCCCGACCCGGCCTCGCCCGACCCGCCCGCCCGCCCCAGAC 840

Qy   841 AGAGCGTTCTTGTAAACTTCTCTCATTATTTGCTACAGAACGGTCTCTGCAAATATTCAGGGGC 900

Qy   901 ATCCCACCCCACCCTGAGCCCTGCCCCTTCCCTCGGGTTTTAGAAAGTGTACAAATCAAA 960

Qy   961 GAACCCGGCCGGTCCTGCGGGGTGGGGCACGCTGGCGGCGCAGACCAGAGGTAACCGGCTCTGC 1020

Qy   1021 GGCCACCTACGGGTCTCAGGAATTACTTGCTAGTGAGAATTACTTGCTAGTGAGCCTTGCGAGCGGCACGTGGGAG 1080

Qy   1081 TCCTATCGACCTCAGAGCCACTATCGATTAGCCCTTAGGGAGTTCCGTCTCTGGGGTCTCCG 1140

Qy   1141 CGGCCTGCGCCCAGTGAGGGGCGCGGGGCGCACCTCCCCGCAGAGCCGGCTTCCCGGCCTTCCCGCCCGCCACCCGG 1199

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTTCTTATCAGGAGGAGGAACTGCTCATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 GCAGATTCCTTAAGCGACCCTTTGGGACAACTTCTTATCAGGAGGAGGAACTGCTCATT 494

Qy   241 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 434

Qy   301 GTGAGGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433 GTGAGGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 374

Qy   361 TCCAGTGCCTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373 TCCAGTGCCTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 314

Qy   421 GGGAACTCCTTTTCCATGAGTACTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 GGGAACTCCTTTTCCATGAGTACTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA 254

Qy   481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 194

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGCCTTGGCCGGGAC--------GCTGGGCGAG 591
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   193 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGCCTTGGCCGGGACGCGGGGGAGCTGGGCGAG 134

Qy   592 CTGGGCCAGCTGACGCGGGGGCGGAGCCACCTCCCCAGAAGCCGGGCTTCCCGCCCACCGG 651
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   133 CTGGGCCAGCTGACGCGGGGGCGGAGCCACCTCCCCAGAAGCCGGGCTTCCCGCCCACCGG 74

Qy   652 ACGTGCCGGCGGGTGGGTAGAGGGGCCGGGCGGGGAGGAGGCTGGCCGGGCGCTC 711
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   73 ACGTGCCGGCGGGTGGGTAGAGGGGCCGGGCGGGGAGGAGGCTGGCCGGGCGCTC 14

Qy   712 GGCAGGGGCGCTCC 724
           ||||||||||||||
Db   13 GGCAGGGGCGCTCC 1

RESULT 4
US-09-925-301-586/c
; Sequence 586, Application US/09925301
; Patent No. US2002005230BA1
GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;   FILE REFERENCE: PA106
;   CURRENT APPLICATION NUMBER: US/09/925,301
;   CURRENT FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: PCT/US00/05882
;   PRIOR FILING DATE: 2000-03-08
;   PRIOR APPLICATION NUMBER: 60/124,270
;   PRIOR FILING DATE: 1999-03-12
;   NUMBER OF SEQ ID NOS: 1694
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 586
;   LENGTH: 1893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1184)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (1865)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (1883)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature

Qy   721 CTCCCCAGCCGTCTCCTCTGCCCCCCTCTTCCTGCCCCGACTCCCCGACCCCGGGGCGCG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 CTCCCCAGCCGTCTCCTCTGCCCCCCTCTTCCTGCCCCGACTCCCCGACCCCGGGGCGCG 420

Qy   781 CGGCCACGCCCCTGCCCTCGCCTCCGGACACCCGCGCCCTGCCCGCCTCGCCCGCCCAGAC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419 CGGCCACGCCCCTGCCCTCGCCTCCGGACACCCGCGCCCTGCCCGCCTCGCCCGCCCAGAC 360

Qy   841 AGAGCGGTTCTTGTAAACTTCTCTTCAGTAGAAAACGTCCTGCTCTCTGAATATTCAGGGGC 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 AGAGCGGTTCTTGTAAACTTCTCTTCAGTAGAAACGGTCCTGCTCTCTGAATATTCAGGGGC 300

Qy   901 ATCCCCACCCTGAGCCTGCCCTTCTCTCGGGTTTGGTTTTAGAAAGTGTACAAATCAAA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 ATCCCCACCCTGAGCCTGCCCTTCTCTCGGGTTTGGTTTTAGAAAGTGTACAAATCAAA 240

Qy   961 GAACCCGGCCGTCCTGCGCGGTGGGGCACGCTGGCGCAGAACCAGAGTAACCGGCTCTGC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 GAACCCGGCCGTCCTGCGCGGTGGGGCACGCTGGCGCAGAACCAGAGTAACCGGCTCTGC 180

Qy   1021 GGCCACCTACGGGTCTAGGAATTACTTGCTGATGACACCCTGCAGGGAGTGGCACGTGGAG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 GGCCACCTACGGGTCTAGGAATTACTTGCTGATGACCCTGCAGGGAGTGGCACGTGGAG 120

Qy   1081 TCCTATCGACCTCAGAGACCACTATCAGATTAGCCCTAGGAGTCCGTCTGGGGTCTCGG 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 TCCTATCGACCTCAGAGACCACTATCAGATTAGCCCTAGGAGTCCGTCTGGGGTCTCGG 60

Qy   1141 CGGCCTGCGCCCAGTGAGGGGCGGACCACCTCCCCAGAAGCCGGGCTTCCCGCCCACCGG 1199
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59   CGGCCTGCGCCCAGTGAGGGGCGGCGCACCTCCCCAGAAGCCGGGCTTCCCGCCCACCGG 1

RESULT 3
US-10-044-090-1/c
; Sequence 1, Application US/10044090
GENERAL INFORMATION:
;   Publication No. US2002013708lA1
;   SOFTWARE: PERL Program
;   APPLICANT: Olga Bandman
;   TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
;   FILE REFERENCE: PA-0028 US
;   CURRENT APPLICATION NUMBER: US/10/044,090
;   CURRENT FILING DATE: 2002-01-09
;   NUMBER OF SEQ ID NOS: 850
;
; SEQ ID NO 1
;   LENGTH: 1124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US2002013708lA1 400788.4
;   NAME/KEY: unsure
;   LOCATION: 1014, 1054, 1119
;   OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-1

Query Match   58.7%; Score 703.4; DB 13; Length 1124;
Best Local Similarity 98.6%; Pred. No. 2.2e-197;
Matches 723; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

Qy   1   GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   733 GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 674

Qy   61   AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   673 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 614

Qy   121 TTTACATTTGCTAAGTGCTAAGTGTCCTGATCTGCTCATGAATCCTTCATGGGGAAGCTGTGGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 TTTACATTTGCTAAGTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG 554

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;   LOCATION: (1887)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (1893)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-586

Query Match    52.9%;  Score 634;  DB 9;  Length 1893;
Best Local Similarity  100.0%;  Pred. No. 1.1e-176;
Matches 634;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1836 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 1777

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTGTCAAATGAGAGTTAGATTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1776 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTGTCAAATGAGAGTTAGATTTTATT 1717

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1716 TTTACATTTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCTATGGGGAAGCTGTGGG 1657

Qy    181 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 1597

Qy    241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1596 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 1537

Qy    301 GTGAGGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGGTACTCCTACACTGG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536 GTGAGGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGGTACTCCTACACTGG 1477

Qy    361 TCCAGTTCCTTCATTATTTTGTCCAAGCCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476 TCCAGTTCCTTCATTATTTTGTCCAAGCCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 1417

Qy    421 GGGAACTCCTTTTCCATGAGTACTCTCCAGGTCTCCCCTTGTTAAGTAGCCTTATCCCCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416 GGGAACTCCTTTTCCATGAGTACTCTCCAGGTCTCCCCTTGTTAAGTAGCCTTATCCCCA 1357

Qy    481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGTGTTCCATTTGAGATGGCATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGTGTTCCATTTGAGATGGCATT 1297

Qy    541 TTGGTGTGGTCCGTTGAAGCCTTGAAGCCTGGCGACGCTGGGCGAGCTGGGCGGAG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296 TTGGTGTGGTCCGTTGAAGCCTTGAAGCCTGGCGACGCTGGGCGAGCTGGGCGGAG 1237

Qy    601 CTGGACGCGGGGCGGAGGGCGAGCGGCGCGGGC 634
          |||||||||||||||||||||||||||||||||
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;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 13
;   LENGTH: 1893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1184)..(1184)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1865)..(1865)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1883)..(1883)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1887)..(1887)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1893)..(1893)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-997-003-13

Query Match   52.9%; Score 634; DB 10; Length 1893;
Best Local Similarity 100.0%; Pred. No. 1.1e-176;
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1836 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 1777

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTGTCAAATGAGAGTTAGATTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1776 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTGTCAAATGAGAGTTAGATTTTATT 1717

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1716 TTTACATTTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCTATGGGGAAGCTGTGGG 1657

Qy    181 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 1597

Qy    241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1596 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 1537

Qy    301 GTGAGGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536 GTGAGGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 1477

Qy    361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 1417

Qy    421 GGGAACTCCTTTTCCATGAGTACTCTCCAGGTCTCTTTGTCCATGGCGTGTTCCATTGACGTGTTCCATTTTTATCCCCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416 GGGAACTCCTTTTCCATGAGTACTCTCCAGGTCTCTTTGTCCATGGCGTGTTCCATTGACGTGTTCCATTTTTATCCCCA 1357

Qy    481 GCGAATTGTGAAATGTAAACATCATGTTTCATGGCGTGTTCCATTTGAGATGGCATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356 GCGAATTGTGAAATGTAAACATCATGTTTCATGGCGTGTTCCATTTGAGATGGCATT 1297

Qy    541 TTGGTGGTCCGTTGGTCGGTGGTCCGTTGAAGCCTTGAAGCCGGCGACGCTGGGCGAGCTGGGGCGAG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296 TTGGTGGTCCGTTGGTCGGTGGTCCGTTGAAGCCTTGAAGCCGGCGACGCTGGGCGAGCTGGGGCGAG 1237

Qy    601 CTGGACGCGGGGCGGAGGGCGAGCGGCGCGGGC 634
          |||||||||||||||||||||||||||||||||
```

Db   1236 CTGGACGCGGGGCGGGAGAGGCGAGCGCGCGGGC 1203

RESULT 6
US-09-880-107-2350/c
; Sequence 2350, Application US/09880107
; Patent No. US2002014298lA1
; GENERAL INFORMATION:
;   APPLICANT: Horne, Darci T.
;   APPLICANT: Vockley, Joseph G.
;   APPLICANT: Scherf, Uwe
;   APPLICANT: Gene Logic, Inc.
;   TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;   FILE REFERENCE: 44921-5028-WO.
;   CURRENT APPLICATION NUMBER: US/09/880,107
;   CURRENT FILING DATE: 2001-06-14
;   PRIOR APPLICATION NUMBER: US 60/211,379
;   PRIOR FILING DATE: 2000-06-14
;   PRIOR APPLICATION NUMBER: US 60/237,054
;   PRIOR FILING DATE: 2000-10-02
;   NUMBER OF SEQ ID NOS: 3950
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2350
;   LENGTH: 649
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US2002014298lA1 M38591
US-09-880-107-2350

Query Match   50.1%; Score 601; DB 9; Length 649;
Best Local Similarity   99.7%; Pred. No. 3.7e-167;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy   1 GGAACTAAAAAAGAACTTATTTATTGAGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 GGAACTAAAAAAGAACTTATTTATTGAGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 AAGCTTATCTGGTATTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTTTATCAGGGAGGAGGGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   469 GCAGATTCCTTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGAGGGCGAACTGCTCATT 411

Qy   241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 351

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGAAGCCCACTTGAAGCCCACTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 291

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 231

Qy   421 GGGAACTTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230 GGGAACTTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCA 171

Qy   481 TTGGTGTGGTCCGTTGAAGCCTTGGGCCTGGGCGCGGAGGCGGCGGCGAGCGGTGGGCGAG 540
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   170 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGGGCGGACGCTGGGCGAGCGGTGGGCGAG 110

Qy   601 CTGGACGCGGGGCGGGAGAGGCGAGC 625
          ||||||||||||||||||||||||||
Db   51 CTGGACGCGGGGCGGGAGAGGCGAGC 27

RESULT 7
US-10-172-118-847/c
; Sequence 847, Application US/10172118
; Publication No. US2003022437 4A1
; GENERAL INFORMATION:
;   APPLICANT: Dai, Hongyue
;   APPLICANT: He, Yudong
;   APPLICANT: Linsley, Peter
;   APPLICANT: Mao, Mao
;   APPLICANT: Roberts, Chris
;   APPLICANT: Van 't Veer, Laura
;   APPLICANT: Van de Vijver, Marc
;   APPLICANT: Bernards, Rene
;   TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;   FILE REFERENCE: 9301-175-999
;   CURRENT APPLICATION NUMBER: US/10/172,118
;   CURRENT FILING DATE: 2002-06-14
;   PRIOR APPLICATION NUMBER: 60/380,770
;   PRIOR FILING DATE: 2002-05-14
;   NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 847
;   LENGTH: 649
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NM_002966
;   DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-847

Query Match   50.1%; Score 601; DB 17; Length 649;
Best Local Similarity   99.7%; Pred. No. 3.7e-167;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy   1 GGAACTAAAAAAGAACTTATTTATTTATTGAGGGCAAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 GGAACTAAAAAAGAACTTATTTATTTATTGAGGGCAAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 AAGCTTATCTGGTATTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTTTATCAGGGAGGAGGGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   469 GCAGATTCCTTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGAGGGCGAACTGCTCATT 411

Qy   241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 351

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 291

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 231

Qy   421 GGGAACTTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230 GGGAACTTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCA 171

Qy   481 GCGAATTTGTGAAATGTAAACATCATGTTTCCATTTGAGATGGCATT 540
          |||||||||||||||||||||||||||||||||||||||||||||||

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Db  421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  230 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 171

Db  481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||
Qy  170 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 111

Qy  541 TTGGTGTGGTCCGTTGAAGCTTGGCCGAGGGCGCGGACCGTGGGCGAGCTGGGCGGAG 600
        |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGGCGCGGACCGCTGGGCGAGCTGGGCGGAG 52

Qy  601 CTGGACGCGGGGCGGAGAGGGCGAGC 625
        ||||||||||||||||||||||||||
Db   51 CTGGACGCGGGGCGGAGAGGGCGAGC 27
```

RESULT 9

US-10-487-337-7/c

; Sequence 7, Application US/10487337
; Publication No. US20040248207A1
; GENERAL INFORMATION:
; APPLICANT: Kenji OKUSE
; APPLICANT: Mark BAKER
; APPLICANT: Louis POON
; APPLICANT: John Nicholas WOOD
; APPLICANT: Misbah MALIK-HALL
; TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
; FILE REFERENCE: 117-492 / N.86242A GCW
; CURRENT APPLICATION NUMBER: US/10/487,337
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: PCT/GB02/03852
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: GB 0120238.1
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112)..(402)
; OTHER INFORMATION:
US-10-487-337-7

Query Match 50.1%; Score 601; DB 20; Length 649;
Best Local Similarity 99.7%; Pred. No. 3.7e-167;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy    1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAACAAATCAA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  649 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAACAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTGCTTCCTGATCTGCTCATGAAATCCTT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  589 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTGCTTCCTGATCTGCTCATGAAATCCTT 530

Qy  121 TTTACATTTGCTAAGTGTCCTCATGTCGCTGCTGCTGATCGCTGATCGCTCATGTGTGGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  529 TTTACATTTGCTAAGTGTCCTCATGTCGCTGCTGCTGATCGCTGATCGCTCATGTGTGGG 470

Qy  181 GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
        |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  469 GCAGATTCCTTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 411

Qy  241 TCTGCCTACTTCTTTCCCTTCGCTTCTTCGCTCGTGCTCATGAACTCTTATCAGGCAATG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  410 TCTGCCTACTTCTTTCCCTTCGCTTCTTCGCTCGTGCTCATGAACTCTTATCAGGCAATG 351

Qy  301 GTGAGGCCCGCAATTAGGGAAAGAAGAGCTCTGGAAGCCCACCTTTGGAAGCCCACTTGG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  350 GTGAGGCCCGCAATTAGGGAAAGAAGAGCTCTGGAAGCCCACCTTTGGAAGCCCACTTGG 291

Qy  361 TCCAGTGCCTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  290 TCCAGTGCCTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 231
```

Db 350 GTGAGGCCCGCAATTAGGGAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 291

Qy 361 TCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 290 TCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 231

Qy 421 GGGAACTCCTTTTCTCAGTGTTCCATGAGTAGCCTTTATCCCCA 480
        ||||||||||||||||||||||||||||||||||||||||||||
Db 230 GGGAACTCCTTTTCTCAGTGTTCCATGAGTAGCCTTTATCCCCA 171

Qy 481 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 170 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 111

Qy 541 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGGCGGCGGACGCGGGACGCGGGAGC 600
        ||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db 110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGGCGGCGGACGCGGGAGC 52

Qy 601 CTGGACGCGGGGCGGGAGAGGCGAGC 625
        ||||||||||||||||||||||||||
Db   51 CTGGACGCGGGGCGGGAGAGGCGAGC 27

RESULT 10
US-10-956-157-979/c
; Sequence 979, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 979
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-979

Query Match   50.1%;   Score 601; DB 21; Length 649;
Best Local Similarity   99.7%;   Pred. No. 3.7e-167;
Matches 623;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   2;

Qy   1 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAGGGCAAACAATACAAAAATCAA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 649 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAGGGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGCTTGTCTTGTCAAATGAGAGTTAGATTTTATT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 589 AAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGCTTGTCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy 121 TTTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCATGGGAGGAGCTGTGGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 529 TTTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCATGGGAGGAGCTGTGGG 470

Qy 181 GCAGATTCCTTAAGCGACCCTTTGGGACAACAACTTCTTATCAGGGAGGAGCGAACTGCTCATT 240
        ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 469 GCAGATTCCTTAAGCGACCCTTT-GGGACAACAACTTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy 241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCAATG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 410 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCAATG 351

Qy 301 GTGAGGCCCGCAATTAGGGAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 350 GTGAGGCCCGCAATTAGGGAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 291

Qy 361 TCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||

Db 290 TCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 231

Qy 421 GGGAACTCCTTTTCTCAGTGTTCCATGAGTAGCCTTTATCCCCA 480
        ||||||||||||||||||||||||||||||||||||||||||||
Db 230 GGGAACTCCTTTTCTCAGTGTTCCATGAGTAGCCTTTATCCCCA 171

Qy 481 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 170 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 111

Qy 541 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGGCGGCGGACGCGGGAGC 600
        ||||||||||||||||||||||||| |||||||||||||||||||||
Db 110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGGCGGCGGACGCGGGAGC 52

Qy 601 CTGGACGCGGGGCGGGAGAGGCGAGC 625
        ||||||||||||||||||||||||||
Db   51 CTGGACGCGGGGCGGGAGAGGCGAGC 27

RESULT 11
US-10-956-157-6214/c
; Sequence 6214, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6214
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-6214

Query Match   50.1%;   Score 601; DB 21; Length 649;
Best Local Similarity   99.7%;   Pred. No. 3.7e-167;
Matches 623;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   2;

Qy   1 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAGGGCAAACAATACAAAAATCAA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 649 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAGGGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGCTTGTCTTGTCAAATGAGAGTTAGATTTTATT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 589 AAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGCTTGTCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy 121 TTTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCATGGGAGGAGCTGTGGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 529 TTTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCATGGGAGGAGCTGTGGG 470

Qy 181 GCAGATTCCTTAAGCGACCCTTTGGGACAACAACTTCTTATCAGGGAGGAGCGAACTGCTCATT 240
        ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 469 GCAGATTCCTTAAGCGACCCTTT-GGGACAACAACTTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy 241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCAATG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 410 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCAATG 351

Qy 301 GTGAGGCCCGCAATTAGGGAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 350 GTGAGGCCCGCAATTAGGGAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 291

Qy 361 TCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 290 TCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 231

Qy 421 GGGAACTCCTTTTCTCAGTGTTCCATGAGTAGCCTTTATCCCCA 480
        |||||||||||||||||||||||||||||||||||||||||||

Db   230 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCA 171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481 GCGAATTTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   170 GCGAATTTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATT 111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCCGAGCGCCGGACGCTGGGCGGCGAG 600
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGCCGGACGCTGGGCGGCGGCGAG 52
          ||||||||||||||||||||||||||
Qy   601 CTGGACGCGGGGCGGAGAGGGCGAGC 625
          ||||||||||
Db   51   CTGGACGCGGGGCGGAGAGGGCGAGC 27

RESULT 12
US-10-264-049-1114/c
; Sequence 1114, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1114
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (553)..(553)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (602)..(602)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (623)..(623)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (656)..(657)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (661)..(661)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-1114

Query Match   49.7%; Score 595.8; DB 17; Length 663;
Best Local Similarity 99.5%; Pred. No. 1.3e-165;
Matches   597; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   2   GAACTAAAAAAAGAACTTTATTATTGAGGGCAAGGGATGCAAACATACAAAAATCAAA 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GAACTAAAAAAGAACCTTTATTTATTGAGGGCAAGGGATGCAACCAATNCAAAAATCAAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   62   AGCTTATCTGGTATTTAACTTTCTTTTCTTCTGCTTGTCAAATGAGAGTTAGAGATTTTATTT 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGCTTATCTGGTATTTAACTTTTCTTTTCTTCTGCTTGTCAAATGAGAGTTAGAGATTTTATTT 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   122 TTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGG 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGG 422

Db   182 CAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGGCGAACTGCTCATT 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 CAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGGCGAACTGCTCATTT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 CTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGG 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 CTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   302 TGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGGT 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 TGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGGT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   362 CCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAG 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 CCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAG 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422 GGAACTCCTTTTCCATGAGTACTCTCAGGTCTCCTTTGTTAAGTAGCCTTTATCCCCAG 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 GGAACTCCTTTTCCATGAGTACTCTCAGGTCTCCTTTGTTAAGTAGCCTTTATCCCCAG 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482 CGAATTGTGAAATGTAAACATCATGGTTCCATTGGATGGTGTTCCATTTGAGATGGCATT 541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CGAATTGTGAAATGTAAACATCATGGTTCCATTGGATGGTGTTCCATTTGAGATGGCATT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542 TGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGCCGAGCGCCGGGCGAGC 601
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601 TGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGCCGAGCGCCGGGCGAGC 2
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   TGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGCCGAGCGCCGGGCGAGC 2

RESULT 13
US-10-027-632-261591/c
; Sequence 261591, Application US/10027632
; Publication No. US2002019871A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261591
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261591

Query Match   48.2%; Score 577.4; DB 13; Length 608;
Best Local Similarity 97.0%; Pred. No. 3.6e-160;
Matches   587; Conservative   1; Mismatches   17; Indels   0; Gaps   0;

Qy   532 GATGGCATTTGGTGTGTCCGTTGAAGCCTTGGCCGAGGCGCCGGCGCCGGCGGCCGGAG 591
          |||| ||| ||||||||||||||||||||||||||||||||||||||
Db   605 GAGGGGCGGCGTGGCGCCGGCGGAGCTCACCTTGGCCGAGGCTTGGCCGGACGCGGGCGGCGGGCGGCGGAG 546
          ||||||||||||||||||||||||||
Qy   592 CTGGGCGAGCTGGACGCGGGGCGGCGGGAGAGGCGGAGAGCGGGCGCCGCCTTCCTTAGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   545 CTGGGCGAGCTGGACGCGGGGCGGCGGGAGAGGCGGAGAGCGGGCGCCGCCTTGTGCGCCTTCCTTAGT 486

RESULT 15

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Matches 587;  Conservative 1;  Mismatches 17;  Indels 0;  Gaps 0;

Qy    532 GATGGCATTTGTGTGTCCGTTGAAGCCTTGCCGAGGCGCGGCGGACGCGTGGGCGGAG 591
              |||   |||||||||||||||||
Db    605 GAGGGCGCGTGGGCCGGCGGAGCGCCTGGGCGAGCGCCGGACGCGCGTGGGCGGAG 546

Qy    592 CTTGGGCGAGCTGACGCGGGGCGGAGAGGCGGAGCTTGCGCGGCCTTGTCCGCCTTAGT 651
              ||||||||||||||||||||||||||||||||||||||||||||
Db    545 CTTGGGCGAGCTGACGCGGGGCGGAGAGGCGGAGCTTGCGCGGCCTTGTCCGCCTTAGT 486

Qy    652 ACGTGCGGCGGGTGGGTAGAGGAGGCGGCGGAGCGGGAGAGGCTTGGCGGCGCTC 711
              ||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACGTGCGGCGGGTGGGTAGAGGAGGCGGCGGAGGCGGGAGAGGCTTGGCGGCGGGCTC 426

Qy    712 GGCAGGGGCTCCCCCCAGCCCTGTCTCTCCCCTCTTCCTGCCCCGACTCCCCCGACC 771
              ||||||||||||||||||||||||||||||||||||||||||||
Db    425 GGCAGGGGCGCGCTCCCCCCAGCCCTGTCTCCCCTCTTCCTGCCCCGACTCCCCCGACC 366

Qy    772 CCGGGGCGCGGCGGCCAGCCCTGCCCTCGCTCCCGACCCCGCGCAGAGGCCTCGCCC 831
              ||||||||||||||||||||||||||||||||||||||||||||
Db    365 CCGGGGCGCGGCGGCCAGCCCTGCCCTCGCTCCCGACCCCGCGCAGAGGCCTCGCCC 306

Qy    832 GCCCCAGACAGAGCGTTCTTGTAAACTTCTCTTCAGTAGAAACGGTCCTGCTCTCGAATA 891
              ||||||||||||||||||||||||||||||||||||||||||||
Db    305 GCCCCAGACAGAGCGTTCTTGTAAACTTCTCTTCAGTAGAAACGGTCCTGCTCTCGAATA 246

Qy    892 TTTCAGGGCATCCCACCCTGCCCTTCCTCTCGGGTTTGGTTTTAGAAAGTGTA 951
              ||||||||||||||||||||||||||||||||||||||||||||
Db    245 TTTCAGGGCATCCCACCCTGCCCTTCCTCTCGGGTTTGGTTTTAGAAAGTGTA 186

Qy    952 CAAATCAAAGAACCCGGCCGTCTCGCGGGTGGGCACGCTGCGCGAGAACCAGAGGTAAC 1011
              ||||||||||||||||||||||||||||||||||||||||||||
Db    185 CAAATCAAAGAACCCGGCCGTCTCGCGGGTGGGCACGCTGGGCGCAGAACCAGAGGTAAC 126

Qy   1012 CGGCTCTGCGGCCACTCACGGGTCTAGGAATTACTTGCTGGATGACCCTGCAGGGAGTGG 1071
              ||||||||||||||||||||||||||||||||||||||||||||
Db    125 CGGCTCTGCGGCCACTCACGGGTCTAGGAATTACTTGCTGGATGACCCTGCAGGGAGTGG 66

Qy   1072 CACGTGGAGTCCTATCGACCTCAGAGGCACTATCAGATTCAGATTAGCCCTAGGAGGTCCGTCTGG 1131
              ||||||::||||||||||||||||||||||||||||||||||||
Db     65 CACGTGGAGTCCTATCGACCTCAGAGGCACTATCAGATTCAGATTAGCCCTAGGAGGTCCGTCTGG 6

Qy   1132 GGGTC 1136
              |||||
Db      5 GGGTC 1
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Query Match        48.2%;  Score 577.4;  DB 17;  Length 608;
Best Local Similarity 97.0%;  Pred. No. 3.6e-160;

Qy    652 ACGTGCGGCGGGTGGGTAGAGGAGGCGGCGGAGCGGGAGAGGCTTGGCGGCGGGCTC 711
              ||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACGTGCGGCGGGTGGGTAGAGGAGGCGGCGGAGGCGGGAGAGGCTTGGCGGCGGGCTC 426

Qy    712 GGAGGGGCTCCCCCAGCCCTGTCTCTCCCCTCTTCCTGCCCCGACTCCCCCGACC 771
              ||||||||||||||||||||||||||||||||||||||||||||
Db    425 GGCAGGGGCGCTCCCCCAGCCCTGTCTCCCCTCTTCCTGCCCCGACTCCCCCGACC 366

Qy    772 CCGGGGCGCGGCGGCCAGCCCTGCCCTCGCTCCCGACCCCGCGCAGAGGCCTCGCCC 831
              ||||||||||||||||||||||||||||||||||||||||||||
Db    365 CCGGGGCGCGGCGGCCAGCCCTGCCCTCGCTCCCGACCCCGCGCAGAGGCCTCGCCC 306

Qy    832 GCCCCAGACAGAGCGTTCTTGTAAACTTCTCTTCAGTAGAAACGGTCCTGCTCTCGAATA 891
              ||||||||||||||||||||||||||||||||||||||||||||
Db    305 GCCCCAGACAGAGCGTTCTTGTAAACTTCTCTTCAGTAGAAACGGTCCTGCTCTCGAATA 246

Qy    892 TTTCAGGGCATCCCACCCTGCCCTTCCTCTCGGGTTTGGTTTTAGAAAGTGTA 951
              ||||||||||||||||||||||||||||||||||||||||||||
Db    245 TTTCAGGGCATCCCACCCTGCCCTTCCTCTCGGGTTTGGTTTTAGAAAGTGTA 186

Qy    952 CAAATCAAAGAACCCGGCCGTCTCGCGGGTGGGCACGCTGGGCGCAGAACCAGAGGTAAC 1011
              ||||||||||||||||||||||||||||||||||||||||||||
Db    185 CAAATCAAAGAACCCGGCCGTCTCGCGGGTGGGCACGCTGGGCGCAGAACCAGAGGTAAC 126

Qy   1012 CGGCTCTGCGGCCACTCACGGGTCTAGGAATTACTTGCTGGATGACCCTGCAGGGAGTGG 1071
              ||||||||||||||||||||||||||||||||||||||||||||
Db    125 CGGCTCTGCGGCCACTCACGGGTCTAGGAATTACTTGCTGGATGACCCTGCAGGGAGTGG 66

Qy   1072 CACGTGGAGTCCTATCGACCTCAGAGGCACTATCAGATTCAGATTAGCCCTAGGAGGTCCGTCTGG 1131
              ||||||::|||||||||||||||||||||||||||||||||||
Db     65 CACGTGGAGTCCTATCGACCTCAGAGGCACTATCAGATTCAGATTAGCCCTAGGAGGTCCGTCTGG 6

Qy   1132 GGGTC 1136
              |||||
Db      5 GGGTC 1
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Query Match   44.8%;   Score 537; DB 9; Length 571;
Best Local Similarity 98.7%; Pred. No. 3.3e-148;
Matches 537; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
        |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db 28 GNAACTAAAAAANAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 87

Qy 61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
        |||||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db 88 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTCGCTTGTCAAATGAGAGTTANATTTTATT 147

Qy 121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 148 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 207

Qy 181 GCAGATTCCTAAGCGACCCTTGGGACAACTGCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 208 GCANATTCCTAAGCGACCCTTGGGACAACTGCTTATCAGGGAGGAGGAGCGAACTGCTCATT 267

Qy 241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 268 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 327

Qy 301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 328 GTGAGGCCCGCAATTAGGGAAAAANAAGCTCTGGAAGCCCACTTTGCCATCTNTACACTGG 387

Qy 361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 388 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 447

Qy 421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTAAGTAGCCTTTATCCCCA 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 448 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTAAGTAGCCTTTATCCCCA 507

Qy 481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGTGTCCATTTGAGATGGCATT 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 508 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGTGTCCATTTGANATGGCATT 567

Qy 541 TTGG 544
        ||||
Db 568 TTGG 571

RESULT 16
US-10-033-528-890
; Sequence 890, Application US/10033528
; Publication No. US20020131197A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 890
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 29, 40, 139, 211, 351, 379, 559
; OTHER INFORMATION: n = A,T,C or G
US-10-033-528-890

' Query Match   44.8%;   Score 537; DB 13; Length 571;
' Best Local Similarity 98.7%; Pred. No. 3.3e-148;

Matches 537; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
        |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db 28 GNAACTAAAAAANAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 87

Qy 61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
        |||||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db 88 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTCGCTTGTCAAATGAGAGTTANATTTTATT 147

Qy 121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 148 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 207

Qy 181 GCAGATTCCTAAGCGACCCTTGGGACAACTGCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 208 GCANATTCCTAAGCGACCCTTGGGACAACTGCTTATCAGGGAGGAGGAGCGAACTGCTCATT 267

Qy 241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 268 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 327

Qy 301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 328 GTGAGGCCCGCAATTAGGGAAAAANAAGCTCTGGAAGCCCACTTTGCCATCTNTACACTGG 387

Qy 361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 388 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 447

Qy 421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTAAGTAGCCTTTATCCCCA 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 448 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTAAGTAGCCTTTATCCCCA 507

Qy 481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGTGTCCATTTGAGATGGCATT 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 508 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGTGTCCATTTGANATGGCATT 567

Qy 541 TTGG 544
        ||||
Db 568 TTGG 571

RESULT 17
US-10-099-926-890
; Sequence 890, Application US/10099926
; Publication No. US2003016064A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 890
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 29, 40, 139, 211, 351, 379, 559
; OTHER INFORMATION: n = A,T,C or G
US-10-099-926-890

Query Match   44.8%;   Score 537; DB 16; Length 571;
Best Local Similarity 98.7%; Pred. No. 3.3e-148;
Matches 537; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy    1 GGAACTAAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAA   60
Db   28 GNAACTAAAAAAAANAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAA   87

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT  120
Db   88 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTCTGCTTGTCAAATGAGAGTTANATTTTATT  147

Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG  180
Db  148 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG  207

Qy  181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  240
Db  208 GCANATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  267

Qy  241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  300
Db  268 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  327

Qy  301 GTGAGGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  360
Db  328 GTGAGGGCCCGCAATTAGGGAAAANAAGCTCTGGAAGCCCACTTGCCATCNTACACTGG  387

Qy  361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  420
Db  388 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  447

Qy  421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  480
Db  448 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  507

Qy  481 GCGAATTTGTGAAATGTAAAACATCATGGTTTCCATTGAGATGGCATT  540
Db  508 GCGAATTTGTGAAATGTAAACATCATGTTTCCATTGANATGGCATT  567

Qy  541 TTGG  544
Db  568 TTGG  571
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RESULT 18
US-10-961-527-890
; Sequence 890, Application US/10961527
; Publication No. US20050147615A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C4
; CURRENT APPLICATION NUMBER: US/10/961,527
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US 09/920,300
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/302,051
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/279,763
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/223,283
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 890
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 29, 40, 139, 211, 351, 379, 559

; OTHER INFORMATION: n = A,T,C or G
US-10-961-527-890

Query Match 44.8%; Score 537; DB 22; Length 571;
Best Local Similarity 98.7%; Pred. No. 3.3e-148;
Matches 537; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 19
US-10-242-535A-47618/c
; Sequence 47618, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47618
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Human

US-10-242-535A-47618

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Query Match        43.0%;   Score 516;  DB 17;   Length 538;
Best Local Similarity 98.9%;   Pred. No. 5.3e-142;
Matches  530;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy         8 AAAAAGAACTTTATTTATTTGAGGGCAAGGGATGCAACCAATCAAAAAATCAAAAGCTTA 67
             |||||||||||||||||||||| |||  |||||||||||||||||||||||||||||||||
Db       535 AAAAAGAACTTTATTTATTTGAGGGCAAGGGATGCAACCAATCAAAAAATCAAAAGCTTA 476

Qy        68 TCTGGTATTTAACTTTCTTTCTTCTTGTTCTGTCAAATGAGAGTTAGATTTTATTTTACAT 127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       475 TCTGGTATTTAACTTTCTTTCTTCTTGTTCTGTCAAATGAGAGTTAGATTTTATTTTACAT 416

Qy       128 TTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCATGGGGGAAGCTGTGGGGCAGATT 187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       415 TTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCATGGGGGAAGCTGTGGGGCAGATT 356

Qy       188 CCTTAAGCGACACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCT 247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       355 CCTTAAGCGACACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCT 296

Qy       248 ACTTCTTTCCCTTCGTCTTATCAGTGTACTACAAAAAATAGTCATTGCATGCAATGGTGAGGC 307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       295 ACTTCTTTCCCTTCGTCTTATCAGTGTACTACAAAAAATAGTCATTGCATGCAATGGTGAGGC 236

Qy       308 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       235 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 176

Qy       368 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTTAAGTAGCCTTTATCCCCAGCGAACT 427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       175 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTTAAGTAGCCTTTATCCCCAGCGAACT 116

Qy       428 CCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCAGCGAATT 487
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       115 CCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCAGCGAATT 56

Qy       488 TGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTTG 543
             ||||||||||||||||||||||||||||||||||||||||||| |
Db        55 TGTGAAATGTAAACATCATGG-AACCATGGCGTGTTCCATTTGAGATGGCATTTTG 1
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RESULT 20
US-10-085-783A-47618/c
; Sequence 47618, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
;   APPLICANT: ChondroGene Inc.
;   APPLICANT: Liew, C.C.
;   TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
;   FILE REFERENCE: 4231/2002
;   CURRENT APPLICATION NUMBER: US/10/085,783A
;   CURRENT FILING DATE: 2002-02-28
;   PRIOR APPLICATION NUMBER: US 60/305,340
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: US 60/275,017
;   PRIOR FILING DATE: 2001-03-12
;   PRIOR APPLICATION NUMBER: US 60/271,955
;   PRIOR FILING DATE: 2001-02-28
;   NUMBER OF SEQ ID NOS: 58994
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 47618
;   LENGTH: 538
;   TYPE: DNA
;   ORGANISM: Human
US-10-085-783A-47618

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Query Match        43.0%;   Score 516;  DB 18;   Length 538;
Best Local Similarity 98.9%;   Pred. No. 5.3e-142;
Matches  530;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy         8 AAAAAGAACTTTATTTATTTGAGGGCAAGGGATGCAACAATACAAAAAATCAAAAGCTTA 67
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RESULT 21
US-09-992-600A-1/c
; Sequence 1, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
;   APPLICANT: Tanaka, Hiroaki
;   APPLICANT: Benjamin, Stephane
;   TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;   FILE REFERENCE: 91.US4.DIV
;   CURRENT APPLICATION NUMBER: US/09/992,600A
;   CURRENT FILING DATE: 2001-11-13
;   PRIOR APPLICATION NUMBER: US 09/924,340
;   PRIOR FILING DATE: 2001-08-06
;   PRIOR APPLICATION NUMBER: PCT/IB01/01715
;   PRIOR FILING DATE: 2001-08-06
;   PRIOR APPLICATION NUMBER: US 60/305,456
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: US 60/302,277
;   PRIOR FILING DATE: 2001-06-29
;   PRIOR APPLICATION NUMBER: US 60/298,698
;   PRIOR FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: US 60/293,574
;   PRIOR FILING DATE: 2001-05-25
;   NUMBER OF SEQ ID NOS: 114
;   SOFTWARE: JPatent
;   SEQ ID NO 1
;   LENGTH: 2016
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..1434
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1435..1836
;   FEATURE:
;   NAME/KEY: 3'UTR
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## Left column

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;   LOCATION: 1837..2016
;   FEATURE:
;   NAME/KEY: polyA_signal
;   LOCATION: 1965..1970
;   FEATURE:
;   NAME/KEY: polyA_site
;   LOCATION: 2001..2016
US-09-992-600A-1

Query Match      40.5%;  Score 485.2;  DB 10;  Length 2016;
Best Local Similarity  94.7%;  Pred. No. 1.4e-132;
Matches  502;  Conservative  0;  Mismatches  28;  Indels  0;  Gaps  0;

Qy    73 TATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT  132
          | ||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2012 TTTTTTTTTTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy   133 AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA  192
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1952 AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA 1893

Qy   193 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC  252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1892 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 1833

Qy   253 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCAATGGTCAATGGTGAGGCCCGCA  312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1832 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCAATGGTCAATGGTGAGGCCCGCA 1773

Qy   313 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC  372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1772 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy   373 ATTATTTGTCCACAGCCAGAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT  432
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1712 ATTATTTGTCCACAGCCAGAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy   433 TCCATGAGTAGTCCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA  492
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Db  1652 TCCATGAGTAGTCCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 1593

Qy   493 AATGTAAACATCATGGTTTCCATTTGAGATGGCATTTGGTGTGTGTCC  552
          ||||||||||||||||||||||||||||||||||||||||||||
Db  1592 AATGTAAACATCATGGTTTCCATTTGAGATGGCATTTGGTGTGTGTCC 1533

Qy   553 GTTGAAGCCTTGGCCCAGGCGCGGCGACGCTGGGCGAGCTGGGCGAGCT  602
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Db  1532 GTTGAAGCCACCAGAGGCTCAGTGCGAGGTCTGGGCAGGCAAGAAAAGGT 1483
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RESULT 22
US-09-924-340-1/c
; Sequence 1, Application US/09924340
; Publication No. US2003002724B A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 1
; LENGTH: 2016

Right column

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..1434
;   NAME/KEY: CDS
;   LOCATION: 1435..1836
;   NAME/KEY: 3'UTR
;   LOCATION: 1837..2016
;   NAME/KEY: polyA_signal
;   LOCATION: 1965..1970
;   NAME/KEY: polyA_site
;   LOCATION: 2001..2016
US-09-924-340-1

Query Match      40.5%;  Score 485.2;  DB 10;  Length 2016;
Best Local Similarity  94.7%;  Pred. No. 1.4e-132;
Matches  502;  Conservative  0;  Mismatches  28;  Indels  0;  Gaps  0;

Qy    73 TATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT  132
          | ||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2012 TTTTTTTTTTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy   133 AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA  192
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1952 AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA 1893

Qy   193 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC  252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1892 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 1833

Qy   253 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCAATGGTCAATGGTGAGGCCCGCA  312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1832 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCAATGGTCAATGGTGAGGCCCGCA 1773

Qy   313 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC  372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1772 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy   373 ATTATTTGTCCACAGCCAGAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT  432
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1712 ATTATTTGTCCACAGCCAGAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy   433 TCCATGAGTAGTCCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA  492
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1652 TCCATGAGTAGTCCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 1593

Qy   493 AATGTAAACATCATGGTTTCCATTTGAGATGGCATTTGGTGTGTGTCC  552
          ||||||||||||||||||||||||||||||||||||||||||||
Db  1592 AATGTAAACATCATGGTTTCCATTTGAGATGGCATTTGGTGTGTGTCC 1533

Qy   553 GTTGAAGCCTTGGCCCAGGCGCGGCGACGCTGGGCGAGCTGGGCGAGCT  602
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Db  1532 GTTGAAGCCACCAGAGGCTCAGTGCGAGGTCTGGGCAGGCAAGAAAAGGT 1483
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RESULT 23
US-09-992-095B-1/c
; Sequence 1, Application US/09992095B
; Publication No. US2003015748SA1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US5.DIV
; CURRENT APPLICATION NUMBER: US/09/992,095B
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13

Publication No. US20030170628A1
GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: G-091US08DIV
; CURRENT APPLICATION NUMBER: US/09/999,570
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent

SEQ ID NO 1
; LENGTH: 2016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..1434
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1435..1836
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1837..2016
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1965..1970
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2001..2016
US-09-999-570-1

Query Match   40.5%;   Score 485.2;   DB 10;   Length 2016;
Best Local Similarity 94.7%;   Pred. No. 1.4e-132;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy   73 TATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 132
                ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2012 TTTTTTTTTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy   133 AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATTCCTTA 192
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1952 AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATTCCTTA 1893

Qy   193 AGGGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 252
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1892 AGGGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 1833

Qy   253 TTTCCCTTCTGCTTGTCATGTGTACTACAAAATAGTCATTGCAATGGTGAGGCCCGCA 312
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Db   1832 TTTCCCTTCTGCTTGTCATGTGTACTACAAAATAGTCATTGCAATGGTGAGGCCCGCA 1773

Qy   313 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1772 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy   373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 432
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Db   1712 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy   433 TCCATGAGTACTCTCAGGTCCTCCTTTGTTGTTAAGTAGCCTTTATCCCCAGCCTTTGTGA 492
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1652 TCCATGAGTACTCTCAGGTCCTCCTTTGTTGTTAAGTAGCCTTTATCCCCAGCCTTTGTGA 1593

Qy   493 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 552
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Db   1592 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 1533

Qy   553 GTTGAAGCCTTGGCCGAGGCGGCGGCGACGCCTGGGCGAGCTGGGCGAGCT 602
            ||||||||||||||||||||||||| ||| || || ||
Db   1532 GTTGAAGCCTTGGCCGAGGCGGCGGCGACGCCTGGGCGAGCTGGGCGAGCAAGAAAGGT 1483

RESULT 24
US-09-999-570-1/c
; Sequence 1, Application US/09999570

Db   1652 TCCATGAGTACTCTCAGTCCTCCCTTTGTGTTAAGTAGCCTTTATCCCAGCGAATTTGTGA 1593
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   493 AATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATTTGTGTGGTCC 552
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Db   1592 AATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATTTGTGTGGTCC 1533

Qy   553 GTTGAAGCCTTGGCCGGAGGCGCCGCGGACGCTGGGCGAGCTGGGGCGAGCT 602
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Db   1532 GTTGAAGCCACCAGAGGCTCAGTGCGAGGTCTGGGCAGGCAAGAAAAGGT 1483

RESULT 25
US-10-000-489-1/c
; Sequence 1, Application US/10000489
; Publication No. US2003092011A1
; GENERAL INFORMATION:
;   APPLICANT: Benjanin, Stephane
;   APPLICANT: Tanaka, Hiroaki
;   TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;   FILE REFERENCE: 91.US6.DIV
;   CURRENT APPLICATION NUMBER: US/10/000,489
;   CURRENT FILING DATE: 2001-11-14
;   PRIOR APPLICATION NUMBER: US 09/924,340
;   PRIOR FILING DATE: 2001-08-06
;   PRIOR APPLICATION NUMBER: PCT/IB01/01715
;   PRIOR FILING DATE: 2001-08-06
;   PRIOR APPLICATION NUMBER: US 60/305,456
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: US 60/302,277
;   PRIOR FILING DATE: 2001-06-29
;   PRIOR APPLICATION NUMBER: US 60/298,698
;   PRIOR FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: US 60/293,574
;   PRIOR FILING DATE: 2001-05-25
;   NUMBER OF SEQ ID NOS: 112
;   SOFTWARE: JPatent
; SEQ ID NO 1
;   LENGTH: 2016
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..1434
;   NAME/KEY: CDS
;   LOCATION: 1435..1836
;   NAME/KEY: 3'UTR
;   LOCATION: 1837..2016
;   NAME/KEY: polyA_signal
;   LOCATION: 1965..1970
;   NAME/KEY: polyA_site
;   LOCATION: 2001..2016
US-10-000-489-1

Query Match   40.5%;   Score 485.2; DB 14; Length 2016;
Best Local Similarity 94.7%;   Pred. No. 1.4e-132;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy   73 TATTTAACTTTCTTCTCTGCTTGCTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 132
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Db   2012 TTTTTTTTTTTTTTCTTCTCTCGCTTGCTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy   133 AAGTGTCCTGATCGTCGCTCATGAAATCCTTCATGGGGAAGCGTGTGGGCAGATTCCTTA 192
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Db   1952 AAGTGTCCTGATCGTCGCTCATGAAATCCTTCATGGGGAAGCGTGTGGGCAGATTCCTTA 1893

Qy   193 AGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGGCTCATTTCTGCCTACTTC 252
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1892 AGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGGCTCATTTCTGCCTACTTC 1833

Qy   253 TTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 312
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Db   1832 TTTCCCTTCTGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 1773

Db   313 ATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTCCTTC 372
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1772 ATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTCCTTC 1713

Db   373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 432
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1712 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Db   433 TCCATGAGTACTCTCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 492
                ||||||||||||||||||||||||||||||| |||
Qy   1652 TCCATGAGTACTCTCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 1593

Db   493 AATGTAAACATCATGGTTCCATGGCGTGTCCATTTGAGATGGCATTTGGTGTGGTCC 552
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1592 AATGTAAACATCATGGTTCCATGGCGTTCCATTTGAGATGGCATTTGGTGTGGTCC 1533

Db   553 GTTGAAGCCTTGGCCGGAGGCGCCGCGGACGCTGGGCGAGCTGGGGCGAGCT 602
                |||||||||||||||||||||||||||||||||||||||| |||
Qy   1532 GTTGAAGCCACCAGAGGCTCAGTGCGAGGTCTGGGCAGGCAAGAAAAGGT 1483

RESULT 26
US-10-000-986-1/c
; Sequence 1, Application US/10000986
; Publication No. US20030096247A1
; GENERAL INFORMATION:
;   APPLICANT: Benjanin, Stephane
;   APPLICANT: Tanaka, Hiroaki
;   TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;   FILE REFERENCE: 91.US9.DIV
;   CURRENT APPLICATION NUMBER: US/10/000,986
;   CURRENT FILING DATE: 2001-11-14
;   PRIOR APPLICATION NUMBER: US 09/924,340
;   PRIOR FILING DATE: 2001-08-06
;   PRIOR APPLICATION NUMBER: PCT/IB01/01715
;   PRIOR FILING DATE: 2001-08-06
;   PRIOR APPLICATION NUMBER: US 60/305,456
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: US 60/302,277
;   PRIOR FILING DATE: 2001-06-29
;   PRIOR APPLICATION NUMBER: US 60/298,698
;   PRIOR FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: US 60/293,574
;   PRIOR FILING DATE: 2001-05-25
;   NUMBER OF SEQ ID NOS: 112
;   SOFTWARE: JPatent
; SEQ ID NO 1
;   LENGTH: 2016
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..1434
;   NAME/KEY: CDS
;   LOCATION: 1435..1836
;   NAME/KEY: 3'UTR
;   LOCATION: 1837..2016
;   NAME/KEY: polyA_signal
;   LOCATION: 1965..1970
;   NAME/KEY: polyA_site
;   LOCATION: 2001..2016
US-10-000-986-1

Query Match   40.5%;   Score 485.2; DB 14; Length 2016;
Best Local Similarity 94.7%;   Pred. No. 1.4e-132;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy   73 TATTTAACTTTCTTCTCTGCTTGCTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 132
                ||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2012 TTTTTTTTTTTTTTCTTCTCTCGCTTGCTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy   133 AAGTGTCCTGATCGTCGCTCATGAAATCCTTCATGGGGAAGCGTGTGGGCAGATTCCTTA 192
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US-10-154-678-1

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Query Match                    40.5%;   Score 485.2;  DB 16;  Length 2016;
Best Local Similarity          94.7%;   Pred. No. 1.4e-132;
Matches  502;  Conservative     0;   Mismatches  28;   Indels    0;   Gaps    0;

Qy    73 TATTTAACTTTCTTCTCGCTGTCAAATGAGAGTTAGATTTATTTTACATTTGCT  132
         ||||   ||||||||||||||||||||  |||||||||||||||  ||||||||||
Db  2012 TTTTTTTTTTTCTTCTCGCTGTCAAATGAGAGTTAGATTTATTTTATTTTACATTTGCT 1953

Qy   133 AAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGCAGATTCCTTA  192
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1952 AAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGCAGATTCCTTA 1893

Qy   193 AGCGACCCTTTGGGACAACTCCTATCAGGAGGAGGGAACTGCTCATTTCTGCCTACTTC  252
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1892 AGCGACCCTTTGGGACAACTCCTATCAGGAGGAGGGAACTGCTCATTTCTGCCTACTTC 1833

Qy   253 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA  312
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1832 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 1773

Qy   313 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC  372
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1772 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy   373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT  432
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1712 ATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy   433 TCCATGAGTACTCTCAGGTCCTCCTTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA  492
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1652 TCCATGAGTACTCTCAGGTCCTCCTTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 1593

Qy   493 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTGTGTGTGTCC  552
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1592 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTGTGTGTGTCC 1533

Qy   553 GTTGAAGCCTTGGCCGAGGCGCCGGCGCCGGCGCCGGCGCTGGGCGAGCTGGGGCGAGCT  602
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Db  1532 GTTGAAGCCACCAGAGCTCAGTGCGAGGTCGGGCGAGGCAAGAAAGGT 1483
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RESULT 28
US-10-001-142-1/c
; Sequence 1, Application US/10001142
; Publication No. US20030198954A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US7.DIV
; CURRENT APPLICATION NUMBER: US/10/001,142
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 1
; LENGTH: 2016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..1434
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1435..1836
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1837..2016

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Db  1952 AAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGCAGATTCCTTA 1893
Qy   193 AGCGACCCTTTGGGACAACTCCTATCAGGAGGAGGGAACTGCTCATTTCTGCCTACTTC  252
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1892 AGCGACCCTTTGGGACAACTCCTATCAGGAGGAGGGAACTGCTCATTTCTGCCTACTTC 1833

Qy   253 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA  312
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1832 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 1773

Qy   313 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC  372
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Db  1772 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy   373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT  432
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Db  1712 ATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy   433 TCCATGAGTACTCTCAGGTCCTCCTTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA  492
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1652 TCCATGAGTACTCTCAGGTCCTCCTTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 1593

Qy   493 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTGTGTGTGTCC  552
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1592 AATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTGTGTGTGTCC 1533

Qy   553 GTTGAAGCCTTGGCCGAGGCGCCGGCGCCGGCGCCGGCGCTGGGCGAGCTGGGGCGAGCT  602
         ||||||||||||||||||      |||    |||   ||
Db  1532 GTTGAAGCCACCAGAGCTCAGTGCGAGGTCGGGCGAGGCAAGAAAGGT 1483
```

RESULT 27
US-10-154-678-1/c
; Sequence 1, Application US/10154678
; Publication No. US2003016218A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 182.US1.REG
; CURRENT APPLICATION NUMBER: US/10/154,678
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 1
; LENGTH: 2016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..1434
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1435..1836
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1837..2016
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1965..1970
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2001..2016
;
```
Db  1952 AAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGCAGATTCCTTA 1893
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;     SOFTWARE: JPatent
;     SEQ ID NO 1
;     LENGTH: 2016
;     TYPE: DNA
;     ORGANISM: Homo sapiens
;     FEATURE:
;     NAME/KEY: 5'UTR
;     LOCATION: 1..1434
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1435..1836
;     FEATURE:
;     NAME/KEY: 3'UTR
;     LOCATION: 1837..2016
;     FEATURE:
;     NAME/KEY: polyA_signal
;     LOCATION: 1965..1970
;     FEATURE:
;     NAME/KEY: polyA_site
;     LOCATION: 2001..2016
US-10-838-854-1
```

Query Match   40.5%;   Score 485.2; DB 21; Length 2016;
Best Local Similarity   94.7%;   Pred. No. 1.4e-132;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```
Qy      73  TATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTTGCT  132
            |||||   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2012  TTTTTTTTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy     133  AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA  192
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1952  AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA 1893

Qy     193  AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC  252
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1892  AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 1833

Qy     253  TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA  312
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1832  TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 1773

Qy     313  ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC  372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1772  ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy     373  ATTATTTTGTCCACAGCCAGAGGGTCTTTCCCTTTGTTAAGTAGCCTTTATCCCCAGCGA  432
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1712  ATTATTTTGTCCACAGCCAGAGGGTCTTTCCCTTTGTTAAGTAGCCTTTATCCCCAGCGA 1653

Qy     433  TCCATGAGTACTCTCAGTCCTCCTTTGATTTTCCAAAAATCCAGGGAACTCCTTT      432
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1652  TCCATGAGTACTCTCAGTCCTCCTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy     493  AATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC  552
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1592  AATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 1533

Qy     553  GTTGAAGCCTTGGCCGAGGCCGCGGCGACGCTGGGCGAGCTGGGCGAGCT      602
            ||||     |||||  ||||||    |||||||||||||||||||||
Db    1532  GTTGAAGCCACCAGAGAGCTCAGTGCGAGGTCTGGGCAGGCAAGAAAGGT 1483
```

```
RESULT 30
US-10-242-535A-46392/c
; Sequence 46392, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
```

NAME/KEY: polyA_signal
LOCATION: 1965..1970
NAME/KEY: polyA_site
LOCATION: 2001..2016
US-10-001-142-1

Query Match   40.5%;   Score 485.2; DB 16; Length 2016;
Best Local Similarity   94.7%;   Pred. No. 1.4e-132;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```
Qy      73  TATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT  132
            |||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2012  TTTTTTTTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy    -133  AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA  192
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1952  AAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA 1893

Qy     193  AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC  252
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1892  AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 1833

Qy     253  TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA  312
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1832  TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 1773

Qy     313  ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC  372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1772  ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy     373  ATTATTTTGTCCACAGCCAGAGGGTCTTTCCCTTTGTTAAGTAGCCTTTATCCCCAGCGA  432
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1712  ATTATTTTGTCCACAGCCAGAGGGTCTTTCCCTTTGTTAAGTAGCCTTTATCCCCAGCGA 1653

Qy     433  TCCATGAGTACTCTCAGTCCTCCTTTGATTTTTCAAAAATCCAGGGAACTCCTTT      432
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1652  TCCATGAGTACTCTCAGTCCTCCTTTGATTTTTCAAAAATCCAGGGAACTCCTTT 1653

Qy     493  AATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC  552
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1592  AATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 1533

Qy     553  GTTGAAGCCTTGGCCGAGGCCGCGGCGACGCTGGGCGAGCTGGGCGAGCT      602
            ||||     |||||  ||||||    |||||||||||||||||||||
Db    1532  GTTGAAGCCACCAGAGAGCTCAGTGCGAGGTCTGGGCAGGCAAGAAAGGT 1483
```

```
RESULT 29
US-10-838-854-1/c
; Sequence 1, Application US/10838854
; Publication No. US2005026182A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/838,854
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US/10/000,489
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
```

; SEQ ID NO 46392
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-46392

Query Match   39.3%;   Score 471.6; DB 18; Length 482;
Best Local Similarity   99.2%;   Pred. No. 7.3e-129;
Matches 474;   Conservative   0; Mismatches 4; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGCGGATCCAAACAATACAAAAATCAA 60
            ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   478 GAACTTAAAAAGAACTTATTATTGAGGGCAAGGGGGTGCAAACAATACAAAAATCAA 419

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   418 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 359

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   358 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 299

Qy   181 GCAGATTCCTTAAGCGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 GCAGATTCCTTAAGCGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 239

Qy   241 TCTGCCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 TCTGCCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 179

Qy   301 GTGAGGCCCGCAATTAGGAGAAAAGAAGCTCTGGAAAGAAGCTCTGGAAGCTGTGGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 GTGAGGCCCGCAATTAGGAGAAAAGAAGCTCTGGAAAGAAGCTCTGGAAGCTGTGGG 119

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 59

Qy   421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCC 478
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCC 1

Query Match   38.5%;   Score 461.4; DB 17; Length 472;
Best Local Similarity   98.7%;   Pred. No. 7.6e-126;
Matches 465;   Conservative   0; Mismatches 6; Indels 0; Gaps 0;

Query Match   39.3%;   Score 471.6; DB 17; Length 482;
Best Local Similarity   99.2%;   Pred. No. 7.3e-129;
Matches 474;   Conservative   0; Mismatches 4; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAGAACTTATTATTGAGGGGATGCAAGGGGATCCAAACAATACAAAAATCAA 60
            || | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   478 GAACTTAAAAAGAACTTATTATTGAGGGCAAGGGGGTGCAAACAATACAAAAATCAA 419

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   418 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 359

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   358 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 299

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 239

Qy   241 TCTGCCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 TCTGCCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 179

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCTCTGGAAGCTCTACACTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCTCTGGAAGCTCTACACTGG 119

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 59

Qy   421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCC 478
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCC 1

RESULT 34
US-10-242-535A-49122/c
; Sequence 49122, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 49122
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-49122

Query Match   37.4%;   Score 448;   DB 17;   Length 480;
Best Local Similarity   95.8%;   Pred. No. 7.2e-122;
Matches   460;   Conservative   0;   Mismatches   20;   Indels   0;   Gaps   0;

```
Qy    3 AACTAAAAAAGAAACTTTATTTATTTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAA  62
          |||||| |||||| |||||||||||||||||||||||||||| ||||| |||||||||||||
Db  480 ACCTAAAAAAGAACCTTTATTTATTTGAGGGCAAGGGGATGCAACCAATCCAAAAATCAAA 421

Qy   63 GCTTATCTGGTATTTAACTTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  420 GCTTATCTGGTATTTAACTTTTCTTTCTCGCTTGCAAATGAGAGTTAGATTTTATTTT 361

Qy  123 TACATTTGCTAAGTGCCTGATCGTCCTGATCGCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGGC 182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  360 TACATTTGCTAAGTGCCTGATCGTCCTGATCGCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGGC 301

Qy  183 AGATTCCTTAAGCAACCTCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTC 242
          ||||||||||||  | ||  ||||||| ||||||||||||||||||||||||||||||||||
Db  300 AGATTCCTTAAGCCGACCCCTTTGGGCAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTC 241

Qy  243 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTTCATGTACTACAAAAATAGTCATTGCAATGGT 302
          |||||||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db  240 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCAATCGT 181
```

RESULT 33
US-10-085-783A-57930/c
; Sequence 57930, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 57930
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57930

Query Match   38.5%;   Score 461.4;   DB 18;   Length 472;
Best Local Similarity   98.7%;   Pred. No. 7.6e-126;
Matches   465;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

```
Qy   73 TATTTAACTTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTGCT 132
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  472 TATTTAACTTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTGCT 413

Qy  133 AAGTGTCCTGATCGTCATGAAATCCTTCATGGGGAAGCTGTGGGGCAGATTCCTTA 192
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  412 AAGTGTCCTGATCGTCATGAAATCCTTCATGGGGAAGCTGTGGGGCAGATTCCTTA 353

Qy  193 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTCTGCCTACTTC 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  352 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTCTGCCTACTTC 293

Qy  253 TTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCAATGGTGAGGCCCGCA 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  292 TTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCAATGGTGAGGCCCGCA 233

Qy  313 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 372
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  232 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 173

Qy  373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 432
          || ||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db  172 GTTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 113

Qy  433 TCCATGAGTACTCTCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 492
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112 TCCATGAGTACTCTCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 53

Qy  493 AATGTAAACATCATGGTTCCATTGAGATGGCATTTG 543
          |||||||||||||||  |||  ||||||||||||||
Db   52 AATGTAAACATCATGGTTCCATTGAGAGGCATTTGG 2
```

RESULT 34 alignment (continued):

```
Db  352 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTCTGCCTACTTC 293

Qy  253 TTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCAATGGTGAGGCCCGCA 312

Db  292 TTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCAATGGTGAGGCCCGCA 233

Qy  313 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 372

Db  232 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC 173

Qy  373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 432

Db  172 GTTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 113

Qy  433 TCCATGAGTACTCTCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 492

Db  112 TCCATGAGTACTCTCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 53

Qy  493 AATGTAAACATCATGGTTCCATTGAGATGGCATTTG 543

Db   52 AATGTAAACATCATGGTTCCATTGAGAGGCATTTGG 2
```

Db   60 GAACTCCTTTCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTTTCCCCAGC   1

RESULT 36
US-10-242-535A-56036/c
; Sequence 56036, Application US/10242535A
; Publication No. US2004013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56036
;   LENGTH: 474
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (432)..(432)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (436)..(436)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-56036

Query Match   37.2%;   Score 446.4; DB 17; Length 474;
Best Local Similarity   98.9%;   Pred. No. 2.1e-121;
Matches 469; Conservative   0; Mismatches   3; Indels   2; Gaps   2;

Qy   9 AAAAGAACTTATTATTATTGAGGGCAAGGGGATGCAAACAAT-ACAAAAATCAAAAGCTTA   67
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   474 AAAAGAACTTATTATTATTGAGGGCAAGGGGATGCAAACAACNCACCNCAAAAATCAAAAGCTTA 415

Qy   68 TCTGGTATTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACAT 127
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   414 TCTGGTATTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACAT 355

Qy   128 TTGCTAAGTGTCCTGATCGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGCAGATT 187
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   354 TTGCTAAGTGTCCTGATCGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGCAGATT 295

Qy   188 CCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCT 247
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   294 CCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCT 235

Qy   248 ACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGC 307
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   234 ACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGC 175

Qy   308 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 367
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   174 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 115

Qy   368 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGGAACT 427
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   114 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGGAACT   55

Qy   428 CCTTTTCCATGAGTACTCTCAGGTCC-TCCTTTGTTAAGTAGCCTTTTTATCCCCA 480
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   54 CCTTTTCCATGAGTACTCTCAGGTCCTTCCTTTGTTAAGTAGCCTTTTTATCCCCA   1

Qy   303 GAGGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 GAGGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 121

Qy   363 CAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGG 422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 CAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGG   61

Qy   423 GAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTTTCCCCAGC 482
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 GAACTCCTTTTCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTTTCCCCAGC   1

RESULT 35
US-10-085-783A-49122/c
; Sequence 49122, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49122
;   LENGTH: 480
;   TYPE: DNA
;   ORGANISM: Human
US-10-085-783A-49122

Query Match   37.4%;   Score 448; DB 18; Length 480;
Best Local Similarity   95.8%;   Pred. No. 7.2e-122;
Matches 460; Conservative   0; Mismatches   0; Indels 20; Gaps   0;

Qy   3 AACTAAAAAGAACTTATTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAA   62
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   480 ACCTAAAAAAGAACTTATTATTATTGAGGGCAAGGGGATGCAAACAACCAATCCAAAAATCAAAA 421

Qy   63 GCTTATCTGGTATTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
            ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   420 GCTTATCTGGTATTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 361

Qy   123 TACATTTGCTAAGTGTCCTGATCGCTCATGAAATCCTTCTATGGGGAAGCTGTGTGGGGC 182
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 TACATTTGCTAAGTGTCCTGATCGCTCATGAAATCCTTCTATGGGGAAGCTGTGTGGGGC 301

Qy   183 AGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTC 242
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 AGATTCCTTAAGCCGCAGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTC 241

Qy   243 TGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGT 302
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 TGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGT 181

Qy   303 GAGGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 GAGGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 121

Qy   363 CAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGG 422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 CAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCAGG   61

Qy   423 GAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTTTATCCCCAGC 482
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 GAACTCCTTTTCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTTTATCCCCAGC 482

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RESULT 37
US-10-085-783A-56036/c
; Sequence 56035, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56036
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (432)..(432)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (436)..(436)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-56036

Query Match             37.2%;   Score 446.4;  DB 18;  Length 474;
Best Local Similarity   98.9%;   Pred. No. 2.1e-121;
Matches  469; Conservative   0; Mismatches   0; Indels   2; Gaps   2;

Qy      9 AAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAAT-ACAAAAATCAAAAGCTTA 67
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    474 AAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACNACCNCAAAAATCAAAAGCTTA 415

Qy     68 TCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACAT 127
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 TCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACAT 355

Qy    128 TTGCTAAGTGTCCTGATCGTCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATT 187
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    354 TTGCTAAGTGTCCTGATCGTCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATT 295

Qy    188 CCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTCTGCCT 247
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 CCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTCTGCCT 235

Qy    248 ACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTGCATGCAATGGTGAGGC 307
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    234 ACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTGCATGCAATGGTGAGGC 175

Qy    308 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 367
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    174 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 115

Qy    368 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACT 427
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    114 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACT 55

Qy    428 CCTTTTCCATGAGTACTCTCAGGTCC-TCCTTTGTTAAGTAGCCTTTATCCCCA 480
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     54 CCTTTTCCATGAGTACTCTCAGGTCCTTCCTTTGTTAAGTAGCCTTTATCCCCA 1

RESULT 38
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US-10-242-535A-56504/c
; Sequence 56504, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56504
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-56504

Query Match             36.2%;   Score 434.4;  DB 17;  Length 448;
Best Local Similarity   99.6%;   Pred. No. 7.5e-118;
Matches  446; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy      1 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAAC-AATACAAAAATCA 59
          ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    448 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCA 389

Qy     60 AAAGCTTATCTGGTATTTAACTTTCTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT 119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 AAAGCTTATCTGGTATTTAACTTTCTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT 329

Qy    120 TTTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGTGG 179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 TTTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGTGG 269

Qy    180 GGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCAT 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 GGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCAT 209

Qy    240 TTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT 299
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT 149

Qy    300 GGTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GGTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG 89

Qy    360 GTCCAGTGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCC 419
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     88 GTCCAGTGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAACC 29

Qy    420 AGGGAACTCCTTTTCCATGAGTACTCTC 447
          ||||||||||||||||||||||||||||
Db     28 AGGGAACTCCTTTTCCATGAGTACTCTC 1

RESULT 39
US-10-085-783A-56504/c
; Sequence 56504, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
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;   CURRENT FILING DATE: 2002-02-28
;   PRIOR APPLICATION NUMBER: US 60/305,340
;   PRIOR FILING DATE: 2001-07-13
;   PRIOR APPLICATION NUMBER: US 60/275,017
;   PRIOR FILING DATE: 2001-03-12
;   PRIOR APPLICATION NUMBER: US 60/271,955
;   PRIOR FILING DATE: 2001-02-28
;   NUMBER OF SEQ ID NOS: 58994
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO 56504
;   LENGTH: 448
;   TYPE: DNA
;   ORGANISM: Human
US-10-085-783A-56504

Query Match        36.2%;   Score 434.4;  DB 18;  Length 448;
Best Local Similarity   99.6%;   Pred. No. 7.5e-118;
Matches  446;   Conservative  0;  Mismatches  1;  Indels  1;  Gaps  1;

Qy    1  GGAACTAAAAAGAACTTTATTATTGAGGGCAAGGGATGCAAAC-AATACAAAAATCA   59
         ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  448  GGAACTAAAAAGAACTTTATTATTGAGGGCAAGGGATGCAAACAAATACAAAAATCA  389

Qy   60  AAAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTAT  119
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  388  AAAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTAT  329

Qy  120  TTTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGG  179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  328  TTTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGG  269

Qy  180  GGCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGAGGAGCCAACTGCTCAT  239
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  268  GGCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGAGGAGCCAACTGCTCAT  209

Qy  240  TTCTGCGCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT  299
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  208  TTCTGCGCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT  149

Qy  300  GGTGAGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG  359
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148  GGTGAGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG   89

Qy  360  GTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCC  419
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88  GTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAAACC   29

Qy  420  AGGGAACTCCTTTCCATGAGTAGTACTCTC  447
         ||||||||||||||||||||||||||||||
Db   28  AGGGAACTCCTTTCCATGAGTAGTACTCTC    1
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RESULT 40
US-09-918-995-21508/c
; Sequence 21508, Application US20030073623A1
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc.
;   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;   TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;   FILE REFERENCE: 20411-756
;   CURRENT APPLICATION NUMBER: US/09/918,995
;   CURRENT FILING DATE: 2001-07-30
;   PRIOR APPLICATION NUMBER: US/09/235,076
;   PRIOR FILING DATE: 1999-01-20
;   NUMBER OF SEQ ID NOS: 38054
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 21508
;   LENGTH: 477
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(477)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-21508

Query Match        35.8%;   Score 429.4;  DB 10;  Length 477;
Best Local Similarity   99.8%;   Pred. No. 2.3e-116;
Matches  430;   Conservative  0;  Mismatches  0;  Indels  1;  Gaps  0;

Qy   92  TGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTGCTAAGTGTCCTGATCTGCTCA  151
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  477  TGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTGCTAAGTGTCCTGATCTGCTCA  418

Qy  152  TGAAATCCTTCTATGGGGAAGCTGTGGGCAGATTCCTTAAGCGACCCTTTGGGACAAC  211
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  417  TGAAATCCTTCTATGGGGAAGCTGTGGGCAGATTCCTTAAGCGACCCTTTGGGACAAC  358

Qy  212  TCTTATCAGGGAGGAGCCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGT  271
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  357  TCTTATCAGGGAGGAGCCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGT  298

Qy  272  GTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCT  331
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  297  GTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCT  238

Qy  332  GGAAGCCCACTTGCCATCTCTCACACTGGTCCAGGTCCTTCAGTCCTTCCACAGCCA  391
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  297  GGAAGCCCACTTGCCATCTCTCACACTGGTCCAGGTCCTTCAGTCCTTCCACAGCCA  178

Qy  332  GGAAGCCCACTTGCCATCTCTCACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCA  391
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  237  GGAAGCCCACTTGCCATCTCTCACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCA  178

Qy  392  GAGGGTCTTTTGATTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGT  451
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  177  GAGGGTCTTTTGATTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGT  118

Qy  452  CCTCCTTGTAAGTAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGGTTT  511
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  117  CCTCCTTGTAAGTAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGGTTT   58

Qy  512  CCATGGCGTGT  522
         ||||||||||
Db   57  CCATGGCGTCT   47
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RESULT 41
US-09-918-995-12556/c
; Sequence 12556, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc.
;   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;   TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;   FILE REFERENCE: 20411-756
;   CURRENT APPLICATION NUMBER: US/09/918,995
;   CURRENT FILING DATE: 2001-07-30
;   PRIOR APPLICATION NUMBER: US/09/235,076
;   PRIOR FILING DATE: 1999-01-20
;   NUMBER OF SEQ ID NOS: 38054
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 12556
;   LENGTH: 466
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(466)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-12556

Query Match        35.2%;   Score 422;  DB 10;  Length 466;
Best Local Similarity   100.0%;   Pred. No. 3.6e-114;
Matches  422;   Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  125  CATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAG  184
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  466  CATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAG  407
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Qy     185  ATTCCTTAAGCGACCCTTTGGGACAACTTCTTATCAGGGAGGAGGAGGCGAACTGCTCATTTCTG  244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     406  ATTCCTTAAGCGACCCTTTGGGACAACTTCTTATCAGGGAGGAGGAGGCGAACTGCTCATTTCTG  347

Qy     245  CCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAATAGTCATTGCATGCAATGGTGA  304
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     346  CCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAATAGTCATTGCATGCAATGGTGA  287

Qy     305  GGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGGTCCA  364
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     286  GGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGGTCCA  227

Qy     365  GGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGA  424
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     226  GGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGA  167

Qy     425  ACTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGA  484
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     166  ACTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGA  107

Qy     485  ATTTGTGAAATGTAAACATCATGGTTTCCATGCGTGTTCCATTTGAGATGGCATTTTGG  544
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     106  ATTTGTGAAATGTAAACATCATGGTTTCCATGCGTGTTCCATTTGAGATGGCATTTTGG  47

Qy     545  TG  546
            ||
Db     46   TG  45
```

RESULT 42
US-09-997-003-26/c
; Sequence 26, Application US/09997003
; Publication No. US20030203361A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA003P1
; CURRENT APPLICATION NUMBER: US/09/997,003
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: unassigned
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/US00/22157
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,680
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-003-26

Query Match   34.3%; Score 411; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.4e-111;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1  GGAACTAAAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418  GGAACTAAAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA  359

Qy      61  AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358  AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  299

Qy     121  TTTACATTGCTAAGTGTCCTGATCGTCATGCATGCAAATCCTTCATGGGGGAAGCTGTGGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298  TTTACATTGCTAAGTGTCCTGATCGTCATGCATGCAAATCCTTCATGGGGGAAGCTGTGGG  239

Qy     181  GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCTGCAACTGCTCATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238  GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCTGCAACTGCTCATT  179
```

```
Qy     241  TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAATAGTCATTGCATGCAATG  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178  TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAATAGTCATTGCATGCAATG  119

Qy     301  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTCG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTCG  59

Qy     361  TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCC  411
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58   TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCC  8
```

RESULT 43
US-10-106-698-2418/c
; Sequence 2418, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2418
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (337)..(337)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (340)..(340)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (348)..(348)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (355)..(355)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (359)..(359)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (365)..(366)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (369)..(369)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (380)..(380)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (463)..(463)
; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (577)..(577)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (584)..(584)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (593)..(593)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (595)..(595)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (621)..(621)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-2418

Query Match   33.0%; Score 396.2; DB 15; Length 632;
Best Local Similarity   95.7%; Pred. No. 1.9e-106;
Matches   424; Conservative   0; Mismatches 16; Indels   3; Gaps   2;

Qy   1 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
              ||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db   512 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAACCAATNCAAAAATCAA 453

Qy   61 AAGCTTATCTGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   452 AAGCTTATCTGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 393

Qy   121 TTTACATTTGCT--AAGTGTCCTGAT--CTGCTCATGAAATCCTTCATGGGGAAGCTGT 177
              |||||||||||| |||||||||| | |||||||||||||||||||||||
Db   392 TTTACATTTGCTNAAGTGTCCTGNTTNNGGTCCTNAANTCCTTTNTATGGGGNAANCTGT 333

Qy   178 GGGGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGGCGAACTGCTC 237
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   332 GGGGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGAGGAGGAACTGCTC 273

Qy   238 ATTTCTGCCTACTTCTTTCCCTCTGCTTCATGTACTACAAAAATAGTCATTGCATGCA 297
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   272 ATTTCTGCCTACTTCTTTCCCTCTGCTTCATGTGCTACACAAAATAGTCATTGCATGCA 213

Qy   298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACAC 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   212 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACAC 153

Qy   358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAT 417
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   152 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAT 93

Qy   418 CCAGGGAACTCCTTTTCCATGAG 440
              |||||||||||||||||||||||
Db   92 CCAGGGAACTCCTTTTCCATGAG 70

RESULT 44
US-10-242-535A-45565/c
; Sequence 45565, Application US/10242535A1
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45565
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-45565

Query Match   31.5%; Score 377.4; DB 17; Length 392;
Best Local Similarity   99.5%; Pred. No. 5.5e-101;
Matches   389; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy   1 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 332

Qy   61 AAGCTTATCTGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 AAGCTTATCTGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 272

Qy   121 TTTACATTTGCTAAGTGTCCTGATCGTGCTCATGAAATCCTTCATGGGGAAGCTGT-GG 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   271 TTTACATTTGCTAAGTGTCCTGATCGTGCTCATGAAATCCTTCATGGGGAAGCTGTCGG 212

Qy   180 GGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGACTGCTCAT 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGACTGCTCAT 152

Qy   240 TTCTGCCTACTTCTTTCCCTCTGCTTCATGTACTACAAAAATAGTCATTGCATGCAAT 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 TTCTGCCTACTTCTTTCCCTCTGCTTCATGTACTACAAAAATAGTCATTGCATGCAAT 92

Qy   300 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCCTACACTG 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   91 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCCTACACTG 32

Qy   360 GTCCAGGTCCTTCATTATTTTGTCCACAGCC 390
              |||||||||||||||||||||||||||||||
Db   31 GTCCAGGTCCTTCATTATTTTGTCCACAGCC 1

RESULT 45
US-10-085-783A-45565/c
; Sequence 45565, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45565
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-45565

Query Match   31.5%; Score 377.4; DB 18; Length 392;
Best Local Similarity   99.5%; Pred. No. 5.5e-101;
Matches   389; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

```
Qy      1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GAAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  332

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 AAGCTTATCTGGTATTTAACTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  272

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGT-GG  179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    271 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTCGG  212

Qy    180 GGCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT  239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GGCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT  152

Qy    240 TTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAAT  299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 TTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAAT   92

Qy    300 GGTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG  359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 GGTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCCACTTTGCCATCTCTACACTG   32

Qy    360 GTCCAGGTCCTTCATTATTTTGTCCACAGCC  390
          |||||||||||||||||||||||||||||||
Db     31 GTCCAGGTCCTTCATTATTTTGTCCACAGCC    1
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Search completed: August 18, 2005, 03:47:45
Job time : 804 secs

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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      August 17, 2005, 22:33:12 ; Search time 5198 Seconds
                                (without alignments)
                             11176.953 Million cell updates/sec

Title:         US-10-735-577-16
Perfect score: 1199
Sequence:    1 ggaactaaaaagaactta..........cgggctcccgcccccaccgg 1199

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0

Searched:    4708233 seqs, 2422760795 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    GenEmbl:*
              1: gb_ba:*
              2: gb_htg:*
              3: gb_in:*
              4: gb_om:*
              5: gb_ov:*
              6: gb_pat:*
              7: gb_ph:*
              8: gb_pl:*
              9: gb_pr:*
             10: gb_ro:*
             11: gb_sts:*
             12: gb_sy:*
             13: gb_un:*
             14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	640.8	53.4	185447	9	AL450992	AL450992 Human DNA
c 2	638	53.2	638	6	CQ715898	CQ715898 Sequence
c 3	637.8	53.2	673	9	BC015973	BC015973 Homo sapi
c 4	601	50.1	649	6	CQ878718	CQ878718 Sequence
c 5	601	50.1	649	6	AR489221	AR489221 Sequence
c 6	601	50.1	649	6	AX409703	AX409703 Sequence
c 7	601	50.1	649	6	AX710164	AX710164 Sequence
c 8	601	50.1	649	6	AX779835	AX779835 Sequence
c 9	601	50.1	649	9	HUMCLANNII	M38591 Homo sapien
c 10	598	49.9	609	9	HUMCALPA1L	M81457 Human calpa
c 11	557	46.5	579	6	AR489209	AR489209 Sequence
c 12	537	44.8	571	6	AX396675	AX396675 Sequence
c 13	530	44.2	646	9	AY179865	AY179865 Macaca mu
c 14	523	43.6	582	6	AX899035	AX899035 Sequence
c 15	523	43.6	582	6	BD034568	BD034568 Sequence
c 16	516	43.0	538	6	CQ702692	CQ702692 Sequence
c 17	485.2	40.5	2016	6	AX616317	AX616317 Sequence
c 18	471.6	39.3	482	6	CQ701466	CQ701466 Sequence
c 19	461.4	38.5	472	6	CQ713004	CQ713004 Sequence
c 20		37.4	448	20	6	CQ704196	CQ704196 Sequence
c 21		37.2	446.4	474	6	CQ711110	CQ711110 Sequence
c 22		36.2	434.4	448	6	CQ711578	CQ711578 Sequence
c 23		36.2	434	604	4	BOVCALPI	M16464 Bovine calp
c 24		35.3	423	434	6	AX777886	AX777886 Sequence
c 25		31.5	389.2	480	9	HUMP11A	M77483 Human p11 p
c 26		31.3	377.4	392	6	CQ700639	CQ700639 Sequence
c 27		31.2	374.2	534	4	AB098817	AB098817 Bos tauru
c 28		30.3	363.6	384	6	CQ709131	CQ709131 Sequence
c 29		29.1	348.8	604	10	BC025044	BC025044 Mus muscu
c 30		28.8	344.8	365	6	CQ706246	CQ706246 Sequence
c 31		28.7	343.6	600	6	AX306168	AX306168 Sequence
c 32		28.7	343.6	600	10	MUSCALPI	M16465 Mouse calpa
c 33		28.6	343	407	6	CQ711127	CQ711127 Sequence
c 34		28.1	337.4	339	6	CQ671113	CQ671113 Sequence
c 35		27.6	330.8	164679	9	AC005921	AC005921 Homo sapi
c 36		27.5	330	330	6	CQ711784	CQ711784 Sequence
c 37		27.5	329.8	600	6	BD251901	BD251901 Potassium
c 38		27.5	329.8	600	6	AR202142	AR202142 Sequence
c 39		27.5	329.8	600	6	AR473726	AR473726 Sequence
c 40		27.5	329.8	600	6	AX407293	AX407293 Sequence
c 41		27.5	329.2	573	6	AX401698	AX401698 Sequence
c 42		27.5	329.2	573	6	AX710160	AX710160 Sequence
c 43		27.5	329.2	573	10	RATS100RP	J03627 Rat S-100 r
c 44		27.4	328.4	570	6	AR489208	AR489208 Sequence
c 45		26.4	317	318	6	AX260435	AX260435 Sequence

```
                          ALIGNMENTS

RESULT 1
AL450992
LOCUS       AL450992            185447 bp    DNA     linear   PRI 18-JAN-2002
DEFINITION  Human DNA sequence from clone RP11-139D23 on chromosome 1, complete
            sequence.
ACCESSION   AL450992 AC024491
VERSION     AL450992.17  GI:18375805
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 185447)
  AUTHORS   Martin,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Jan 25, 2002 this sequence version replaced gi:1616488.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP11-139D23 is from the library RPCI-11.1 constructed by the group
```

```
                                                         Db   155309 GGGTTCTCGGCGGCCGCTGCCGCCAGTGGAGGGGGGGCCACCTCCCCAGAGACCGGGCTTCCCGC 155368
                                                                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                         Qy     1192 CCCACCGG 1199
                                                                     ||||||||
                                                         Db   155369 CCCACCGG 155376

                                             RESULT 2
                                             CQ715898/c
                                             LOCUS       CQ715898               638 bp    DNA       linear   PAT 03-FEB-2004
                                             DEFINITION  Sequence 1832 from Patent WO02068579.
                                             ACCESSION   CQ715898
                                             VERSION     CQ715898.1  GI:42276755
                                             KEYWORDS    .
                                             SOURCE      Homo sapiens (human)
                                             ORGANISM    Homo sapiens
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             REFERENCE   1
                                             AUTHORS     Venter,C.J., Adams,M.C., Li.P.W. and Myers,E.W.
                                             TITLE       Kits, such as nucleic acid arrays, comprising a majority of
                                                         humanexons or transcripts, for detecting expression and other uses
                                                         thereof
                                             JOURNAL     Patent: WO 02068579-A 1832 06-SEP-2002;
                                                         PE Corporation (NY) (US)
                                             FEATURES             Location/Qualifiers
                                                  source          1..638
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                                                                  /mol_type="unassigned DNA"
                                                                  /db_xref="taxon:9606"
                                             ORIGIN
                                             Query Match             53.2%;  Score 638;  DB 6;  Length 638;
                                             Best Local Similarity  100.0%;  Pred. No. 1.5e-125;
                                             Matches   638;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

                                             Qy      1 GGAACTAAAAAGAACTTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAA 60
                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                             Db    638 GGAACTAAAAAGAACTTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAA 579

                                             Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                             Db    578 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 519

                                             Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                             Db    518 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 459

                                             Qy    181 GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                             Db    458 GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 399

                                             Qy    241 TCTGCCTACTTCTTTCCCTTCGCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                             Db    398 TCTGCCTACTTCTTTCCCTTCGCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 339

                                             Qy    301 GTGAGGCCCGCAATTAGGGAGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                             Db    338 GTGAGGCCCGCAATTAGGGAGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 279

                                             Qy    361 TCCAGGTTCCTTCATTATTTTGTCCAGCCAGAGAGGGTTCTTTTGATTTTCCAAAAATCCA 420
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                                             Db    278 TCCAGGTTCCTTCATTATTTTGTCCAGCCAGAGAGGGTTCTTTTGATTTTCCAAAAATCCA 219

                                             Qy    421 GGGAACTTCCTTTGCCATGAGTACTTGCTCCAGGTACCTGCAGGGAGTGG 480
                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||
                                             Db    218 GGGAACTTCCTTTGCCATGAGTACTTGCTCCAGGTACCTGCAGGGAGTGG 159

                                             Qy    481 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT 540
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                                             Db    158 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT 99
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                 of Pieter de Jong. For further details see
                 http://www.chori.org/bacpac/home.htm
                 VECTOR: pBACe3.6
                 This sequence is the entire insert of clone RP11-139D23 The true
                 left end of clone RP11-353M1 is at 85124 in this sequence. The true
                 right end of clone RP11-98D18 is at 22235 in this sequence.
     FEATURES             Location/Qualifiers
          source          1..185447
                          /organism="Homo sapiens"
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                          /chromosome="1"
                          /clone="RP11-139D23"
                          /clone_lib="RPCI-11.1"
          misc_feature    41104..41203
                          /note="Single clone region. Sequence from reads from a
                          short insert library derived from a clone PCR. Restriction
                          digest data confirm the assembly."
          misc_feature    108101..108200
                          /note="Single clone region. Sequence from reads from a
                          short insert library derived from a clone PCR. Restriction
                          digest data confirm the assembly."
          misc_feature    108708..108843
                          /note="Single clone region. Sequence from reads from a
                          short insert library derived from a clone PCR. Restriction
                          digest data confirm the assembly."
     ORIGIN
     Query Match            53.4%;  Score 640.8;  DB 9;  Length 185447;
     Best Local Similarity  97.5%;  Pred. No. 7.3e-126;
     Matches   651;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

     Qy      532 GATGGCATTTGGTGTGGTGGTCCGTTGAAGCTGGCCTTGCCGAGGCGCGGCGGACGTGGGCGAG 591
                 |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
     Db   154709 GAGGGGCGAGCTGGACGCCGGGCCGGGCCGGGCGGAGCTCACCTTGCCGAGGCGCGGCGGACGTGGGCGAG 154768

     Qy      592 CTGGGCGAGCTGGACGCCGGGCCGGGCGGAGCGGCGGCGGGAGCGGCGGGAGCGGCGGCCTGCGCGGCGGCTC 651
                 ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
     Db   154769 CTGGGCGAGCTGGACGCCGGGCCGGGCGGAGCGGCGGCGGGAGCGGCGGGAGCGGCGGCCTGCGCGGCGGCTC 154828

     Qy      652 ACGTGCGGCGGGTGGTAGAGGGAGGAGGCGGCGGCGGAGCGGGAGGAGGCCCTGCGCGGCGCTC 711
                 |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
     Db   154829 ACGTGCGGCGGGTGGTAGAGGGAGGAGGCGGCGGCGGAGCGGGAGGAGGCCCTGCGCGGCGCTC 154888

     Qy      712 GGCAGGGCGGCTCCCCCAGCCTGTCCCCTCCTGCCCCCCCTCTGCCCCCCCGACCCCCCGACC 771
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     Db   154889 GGCAGGGCGGCTCCCCCAGCCTGTCCCCTCCTGCCCCCCCTCTGCCCCCCCGACCCCCCGACC 154948

     Qy      772 CCGGGCGGCGGCGGCGGCCCACGCCCCGCTCCCGGCTCCCGGACCCCCGCTCCCGAGGGCCTCGCCC 831
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db   154949 CCGGGCGGCGGCGGCGGCCCACGCCCCGCTCCCGGCTCCCGGACCCCCGCTCCCGAGGGCCTCGCCC 155008

     Qy      832 GCCCCAGACAGAGAGCGGTTCTTGTAAACTTCTTCTTCAGTAGAAACGGTCCTGCTCTCGAATA 891
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     Db   155009 GCCCCAGACAGAGAGCGGTTCTTGTAAACTTCTTCTTCAGTAGAAACGGTCCTGCTCTCGAATA 155068

     Qy      892 TTTCAGGGCATCCCCCACCCTGAGCCCTGCCCCTTCCTCGGGTTTGGTTTTTAGAAAGTGTA 951
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     Db   155069 TTTCAGGGCATCCCCCACCCTGAGCCCTGCCCCTTCCTCGGGTTTGGTTTTTAGAAAGTGTA 155128

     Qy      952 CAAATCAAAGAACCCGGCCGTCCTGCGGGTGGGGCACGTGGGCACGCGCCTGCCGCAGAACCAGAGCTAAC 1011
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db   155129 CAAATCAAAGAACCCGGCCGTCCTGCGGGTGGGGCACGTGGGCACGCGCCTGCCGCAGAACCAGAGCTAAC 155188

     Qy     1012 CGGCTCTGCGCGCCACTACGGGTCTAGGAATTACTTGCTGGATGACCCTGCAGGGAGTGG 1071
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db   155189 CGGCTCTGCGCGCCACTACGGGTCTAGGAATTACTTGCTGGATGACCCTGCAGGGAGTGG 155248

     Qy     1072 CACGTGGAGTCCTATCGACCTCAGAGGCACTATCAGATTAGCCCTAGGAGGAGTCCGTCTG 1131
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db   155249 CACGTGGAGTCCTATCGACCTCAGAGGCACTATCAGATTAGCCCTAGGAGGAGTCCGTCTG 155308

     Qy     1132 GGGTCTCGGCGGCCGCTGCCGCCAGTGGAGGGGGGGCCACCTCCCCAGAGACCGGGCTTCCCGC 1191
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGCGACGCTGGGCGAGCTGGGCGAG 600
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Db     98  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGCGACGCTGGGCGAGCTGGGCGAG 39

Qy    601  CTGGACGCGCGGCGGCGGAGAGGCGAGGCGAGCGGCGGCGGCGGCTGTG 638
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     38  CTGGACGCGCGGCGGCGGAGAGGCGAGGCGAGCGGCGGCGGCGGCTGTG 1
```

RESULT 3
BC015973/c

LOCUS   BC015973   673 bp   mRNA   linear   PRI 29-JUN-2004
DEFINITION Homo sapiens S100 calcium binding protein A10 (annexin II ligand,
            calpactin I, light polypeptide (p11)), mRNA (cDNA clone MGC:23737
            IMAGE:4103596), complete cds.
ACCESSION   BC015973
VERSION   BC015973.1 GI:16359017
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 673)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED   12477932
REFERENCE   2 (bases 1 to 673)
AUTHORS   Strausberg,R.
TITLE   Direct Submission
JOURNAL   Submitted (22-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
COMMENT   Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 32 Row: e Column: 16.
FEATURES   Location/Qualifiers
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     gene   /tissue_type="Brain, glioblastoma"
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                     /db_xref="MIM:114085"

     CDS   103..396
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                     /codon_start=1
                     /product="S100 calcium-binding protein A10"
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                     /db_xref="GI:16359018"
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                     /translation="MPSQMEHAMETMMFTPHKFAGDKGYLTKEDLRVLMEKEFPGFLE
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Query Match   53.2%; Score 637.8; DB 9; Length 673;
Best Local Similarity 99.7%; Pred. 1.7e-125;
Matches 639;   Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACATACAAAAATCAA 60
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Db   641 GGAACTAAAAAGAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACATACAAAAATCAA 582

Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 AAGCTTATCTGGTATTTAACTTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 522

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGATGAAATCCTTCATGGGGGAAGCGTGGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGATGAAATCCTTCATGGGGGAAGCGTGGG 462

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 402

Qy   241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 342

Qy   301 GTGAGGCCCGCAATTAGGAGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG 360
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Db   341 GTGAGGCCCGCAATTAGGAGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG 282

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 222

Qy   421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA 162

Qy   481 GGGAATTTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
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Db   161 GCGAATTTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATT 102

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGGCGGACCGCTGGGCGAGCTGGGCGAG 600
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Db   101 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGGCGGACCGCTGGGCGAGCTGGGCGAG 42

Qy   601 CTGGACGCGGGGCGGCGGAGAGGCGAGGCGAGCGGCGGCGGGCTGCGC 641
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RESULT 4
CQ878718/c

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LOCUS       CQ878718                 649 bp    DNA     linear   PAT 04-OCT-2004
DEFINITION  Sequence 3 from Patent WO2004080424.
ACCESSION   CQ878718
VERSION     CQ878718.1  GI:53791165
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yeh,L.A., Cuny,G.D., Padmanaban,D. and Ding,K.
  TITLE     Methods and compositions for neurite outgrowth detection
  JOURNAL   Patent: WO 2004080424-A 3 23-SEP-2004;
            THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1..649
                     /organism="Homo sapiens"
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                     /translation="MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLE
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ORIGIN

  Query Match             50.1%;  Score 601;  DB 6;  Length 649;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-117;
  Matches  623;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy          1 GGAACTAAAAAGAAGAACTTTATTTATTGAGGCAAGGGGATGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db        649 GGAACTAAAAAGAAGAACTTTATTTATTGAGGCAAGGGGATGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy         61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db        589 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy        121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
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Db        529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy        181 GCAGATTCCTAAGCGACCCTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
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Db        469 GCAGATTCCTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy        241 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATCATTGCATGCAATG 300
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Db        410 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATCATTGCATGCAATG 351

Qy        301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
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Db        350 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy        361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
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Db        290 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 231

Qy        421 GGGAACTCCTTTCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 480
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Db        230 GGGAACTCCTTTCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 171

Qy        481 GCGAATTTGTGAAATGTAAACATCATGGTTTCATTTGAGATGGCATT 540
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Db        170 GCGAATTTGTGAAATGTAAACATCATGGTTTCATTTGAGATGGCATT 111

Qy        541 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCCGGACGCTGGGCGAG 600
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Qy        601 CTGGACGCGGGGCGGGCGGGAGAGGCGAGC 625
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Db         51 CTGGACGCGGGGCGGGCGGGAGAGGCGAGC 27
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RESULT 5
AR489221/c

LOCUS       AR489221                 649 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 36 from patent US 6709855.
ACCESSION   AR489221
VERSION     AR489221.1  GI:47256166
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Stanton,L.W., White,R.T., Damm,D.L., Lewicki,J.A., Joly,A. and
            Schreiner,G.F.
  TITLE     Methods for detection and use of differentially expressed genes in
            disease states
  JOURNAL   Patent: US 6709855-A 36 23-MAR-2004;
FEATURES             Location/Qualifiers
     source          1..649
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ORIGIN

  Query Match             50.1%;  Score 601;  DB 6;  Length 649;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-117;
  Matches  623;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy          1 GGAACTAAAAAGAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Qy         61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db        589 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy        121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy        181 GCAGATTCCTAAGCGACCCTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        469 GCAGATTCCTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy        241 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATCATTGCATGCAATG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATCATTGCATGCAATG 351

Qy        301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy        361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 231

Qy        421 GGGAACTCCTTTCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GGGAACTCCTTTCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 171

Qy        481 GCGAATTGTGAAATGTAAACATCATGGTTTCATTTGAGATGGCATT 540
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GCGAATTGTGAAATGTAAACATCATGGTTTCATTTGAGATGGCATT 111

Qy        541 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCCGGACGCTGGGCGAG 600
              ||||||||||||||||||||||||| ||||||||||||||||||||
Db        110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCCGGACGCTGGGCGAG 52

Qy        601 CTGGACGCGGGGCGGGCGGGAGAGGCGAGC 625
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Db         51 CTGGACGCGGGGCGGGCGGGAGAGGCGAGC 27
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RESULT 6

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LOCUS       AX409703               649 bp   DNA       linear  PAT 14-JUN-2002
DEFINITION  Sequence 2350 from Patent WO0229103.
ACCESSION   AX409703
VERSION     AX409703.1  GI:21142408
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE       Gene expression profiles in liver cancer
JOURNAL     Patent: WO 0229103-A 2350 11-APR-2002;
            GENE LOGIC INC (US)
FEATURES             Location/Qualifiers
     source          1..649
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="EMBL/GenBank Accession No. M38591"
ORIGIN
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Query Match           50.1%;  Score 601;  DB 6;  Length 649;
Best Local Similarity  99.7%;  Pred. No. 1.2e-117;
Matches   623;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   2;

Qy      1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db    589 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGTGGG 180
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Db    529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGTGGG 470

Qy    181 GCAGATTCCTTAAGCGACCCCTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    469 GCAGATTCCTTAAGCGACCACCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy    241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    410 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 351

Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    350 GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy    361 TCCAGTGCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290 TCCAGTGCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 231

Qy    421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 171

Qy    481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGCGCATT 540
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Db    170 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGCGCATT 111

Qy    541 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGGCGGACCGCTGGGCGGCTGGGCGGAG 600
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Db    110 TTGGTGTGGTCCGTTGAAGCCTTGGCGAGGCGGCGGACCGCTGGGCGGCTGGGCGGAG 52

Qy    601 CTGGACGCGGGGCGGGAGAGGGCGAGC 625
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Db     51 CTGGACGCGGGGCGGGAGAGGGCCAGC 27
```

RESULT 7

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LOCUS       AX710164               649 bp   DNA       linear  PAT 10-APR-2003
DEFINITION  Sequence 7 from Patent WO03016917.
ACCESSION   AX710164
VERSION     AX710164.1  GI:29786759
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Okuse,K., Baker,M., Poon,L., Wood,J.N. and Malik-Hall,M.
TITLE       Sodium channel regulators and modulators
JOURNAL     Patent: WO 0301691-A 7 27-FEB-2003;
            UNIVERSITY COLLEGE LONDON (GB)
FEATURES             Location/Qualifiers
     source          1..649
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                     /db_xref="taxon:9606"
     CDS             112..405
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                     /codon_start=1
                     /protein_id="CAD88531.1"
                     /db_xref="GI:29786760"
                     /translation="MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLE
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ORIGIN
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Query Match           50.1%;  Score 601;  DB 6;  Length 649;
Best Local Similarity  99.7%;  Pred. No. 1.2e-117;
Matches   623;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   2;

Qy      1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db    649 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db    589 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGTGGG 470

Qy    181 GCAGATTCCTTAAGCGACCCCTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    469 GCAGATTCCTTAAGCGACCACCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy    241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    410 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 351

Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
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Db    350 GTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy    361 TCCAGTGCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290 TCCAGTGCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 231

Qy    421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 171

Qy    481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    170 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATT 111

Qy    541 TTGGTGTGGTCCGTTGAAGCCTTGGGCCGGCGGCGGACCGCTGGGCGGCTGGGCGGAG 600
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Db   110 TTGGTGTGGTCCGTTGAAGCCTTGCCGAGGCGCGGCGACGCTGGCGAGCGCGCGCGAGCGCGAGCTGGGCGAGCTGGGCGAG 600
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Qy   541 TTGGTGTGGTCCGTTGAAGCCTTG-CGAGGCGCGGCGACGCTGGCGAGCGCGCGCGAGCGCGAGCTGGGCGAGCTGGGCGAG 52

Db   110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGGCGACGCTGGCGAGCGCGCGCGAGCGCGAGCTGGGCGAGCTGGGCGAG 52

Qy   601 CTGGACGCGGGGCGGGGCCGGAGAGGCGAGC 625
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Db   51 CTGGACGCGGGGCGGGGCCGGAGAGGCGAGC 27

Qy   601 CTGGACGCGGGGCGGGGCCGGAGAGGCGAGC 625
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Db   51 CTGGACGCGGGGCGGGGCCGGAGAGGCGAGC 27

RESULT 9
HUMCLANNII/c
LOCUS   HUMCLANNII   649 bp   mRNA   linear   PRI 31-DEC-1994
DEFINITION Homo sapiens cellular ligand of annexin II (p11) mRNA, complete
            cds.
ACCESSION   M38591
VERSION   M38591.1 GI:180595
KEYWORDS   cellular ligand of annexin II.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 649)
  AUTHORS   Kube,E., Weber,K. and Gerke,V.
  TITLE   Primary structure of human, chicken, and Xenopus laevis p11, a
            cellular ligand of the Src-kinase substrate, annexin II
  JOURNAL   Gene 102 (2), 255-259 (1991)
   MEDLINE 91340161
   PUBMED   1831433
COMMENT   Original source text: Homo sapiens (tissue library: lambda-GT10)
            adenocarcinoma cDNA to mRNA.
            Draft entry and computer-readable sequence for [Unpublished (1990)]
            kindly submitted
            by V.Gerke, 17-SEP-1990.
            Max-Planck-Institute for Biophysical Chemistry
            Dept Biochemistry
            Am Fassberg
            D-3400 Goettingen, FRG.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="adenocarcinoma"
                     /tissue_lib="lambda-GT10"
     gene   1..649
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     CDS   112..405
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                     /protein_id="AAA58426.1"
                     /db_xref="GI:180596"
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ORIGIN

Query Match   50.1%;   Score 601; DB 9; Length 649;
Best Local Similarity   99.7%;   Pred. No. 1.2e-117;
Matches 623; Conservative   0; Mismatches   0; Indels   2; Gaps   2;

Qy   1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
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Db   649 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db   589 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy   589 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Db   110 TTGGTGTGGTCCGTTGAAGCCTTGCCGAGGCGCGGCGACGCTGGCGAGCTGGGCGAG 52
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Qy   601 CTGGACGCGGGGCGGGGCCGGAGAGGCGAGC 625
           |||||||||||||||||||||||||||
Db   51 CTGGACGCGGGGCGGGGCCGGAGAGGCGAGC 27

RESULT 8
AX779835/c
LOCUS   AX779835   649 bp   DNA   linear   PAT 14-JUL-2003
DEFINITION Sequence 1992 from Patent WO03039443.
ACCESSION   AX779835
VERSION   AX779835.1 GI:32696829
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
            Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
  TITLE   Novel genetic markers for leukemias
  JOURNAL   Patent: WO 03039443-A 1992 15-MAY-2003;
            Deutsches Krebsforschungszentrum (DE) ; Haferlach, Torsten,
            Ludwig-Maximilian-Universitaet Muenchen (DE) ; Kern, Wolfgang (DE)
            PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES   Location/Qualifiers
     source   1..649
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   50.1%;   Score 601; DB 6; Length 649;
Best Local Similarity   99.7%;   Pred. No. 1.2e-117;
Matches 623; Conservative   0; Mismatches   0; Indels   2; Gaps   2;

Qy   1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
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Db   649 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db   589 AAGCTTATCTGGTATTTAACTTTCTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy   181 GCAGATTCCTTAAGCCACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCCGAACTGCTCATT 240
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Db   469 GCAGATTCCTTAAGCCACCCTTT-GGACAACTCTTATCAGGGAGGAGGAGCCGAACTGCTCATT 411

Qy   241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTTCATTGCATGCAATG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTTCATTGCATGCAATG 351

Qy   301 GTGAGGCCCCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
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Db   350 GTGAGGCCCCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy   361 TCCAGTGTCCTTCATTATTTTGTCCACAGCCAGGAGGTGCTCTTTGATTTTCCAAAAATCCA 420
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Db   290 TCCAGTGTCCTTCATTATTTTGTCCACAGCCAGGAGGTGCTCTTTGATTTTCCAAAAATCCA 231

Qy   421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCA 480
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Db   230 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCA 171

Qy   481 GCGAATTGTGAAATGTAAACATCATGGTTCCATTGGCGTGTTCCATTTGAGATGCGATT 540
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ORIGIN

     Query Match    49.9%;  Score 598;  DB 9;  Length 609;
     Best Local Similarity  99.8%;  Pred. No. 5.2e-117;
     Matches 609;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy        1 GGAACTAAAAAGAACTTATTTATTGAGGGACGATGCAAACAATACAAAAATCAA    60
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Db      609 GGAACTAAAAAGAACTTATTTATTGAGGGACGATGCAAACAATACAAAAATCAA    550

Qy       61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTTTCTCTTTCTTGAGTTAGATTTTATT   120
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      549 AAGCTTATCTGGTATTTAACTTTCTTTCTCTTGCTTGTCAAATGAGTTAGATTTTATT   490

Qy      121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAGCTGTGGG   180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      489 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAGCTGTGGG   430

Qy      181 GCAGATTCCTTAAGCCACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT   240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      429 GCAGATTCCTTAAGCCACCCTTT-GGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT   371

Qy      241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCATGCAATG   300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCATGCAATG   311

Qy      301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG   360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      310 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG   251

Qy      361 TCCAGGTCCTTCATTATTTGTTAAGTAGCCTTTATCCCCA   420
            ||||||||||||||||||||||||||||||||||||||||
Db      250 TCCAGGTCCTTCATTATTTGTTAAGTAGCCTTTATCCCCA   191

Qy      421 GGGAACTCCTTTTCCATGAGTACTCCTCAGGTCTCCTTTGTTAAGTAGCCTTTATCCCCA   480
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Db      190 GGGAACTCCTTTTCCATGAGTACTCCTCAGGTCTCCTTTGTTAAGTAGCCTTTATCCCCA   131

Qy      481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT   540
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Db      130 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT    71

Qy      541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGCGACCGTGGGCGGAGCTGGGCGGAG   600
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Db       70 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGCGACCGTGGGCGGAGCTGGGCGGAG    11

Qy      601 CTGGACGCGCGG   610
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Db       10 CTGGACGCGCGG     1

RESULT 11
AR489209/c
LOCUS       AR489209            579 bp    DNA         linear    PAT 15-MAY-2004
DEFINITION  Sequence 24 from patent US 6709855.
ACCESSION   AR489209
VERSION     AR489209.1  GI:47256154
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Stanton,L.W., White,R.T., Damm,D.L., Lewicki,J.A., Joly,A. and
            Schreiner,G.F.
  TITLE     Methods for detection and use of differentially expressed genes in
            disease states
  JOURNAL   Patent: US 6709855-A 24 23-MAR-2004;
FEATURES             Location/Qualifiers
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Qy      121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAGCTGTGGG   180
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Db      529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAGCTGTGGG   470

Qy      181 GCAGATTCCTTAAGCCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT   240
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Db      469 GCAGATTCCTTAAGCCGACCCCTTT-GGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT   411

Qy      241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCATGCAATG   300
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Db      410 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATGCATGCAATG   351

Qy      301 GTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG   360
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Db      350 GTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG   291

Qy      361 TCCAGGTCCTTCATTATTTGTCCACAGCCCAGAGGGTCTTTTGATTTTCCAAAAATCCA   420
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Db      290 TCCAGGTCCTTCATTATTTGTCCACAGCCCAGAGGGTCTTTTGATTTTCCAAAAATCCA   231

Qy      421 GGGAACTCCTTTTCCATGAGTACTCCTCAGGTCTCCTTTGTTAAGTAGCCTTTATCCCCA   480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      230 GGGAACTCCTTTTCCATGAGTACTCCTCAGGTCTCCTTTGTTAAGTAGCCTTTATCCCCA   171

Qy      481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT   540
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Db      170 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT   111

Qy      541 TTGGTGTGGTCCGTTGAAGCCTTGGGCCGGGGGGCGGCGGACCGTGGGCGGAGCTGGGCGGAG   600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGGCGGCGGACCGTGGGCGGAGCTGGGCGGAG    52

Qy      601 CTGGACGCGCGGCGGGAGGGCGAGC   625
            ||||||||||||||||||||
Db       51 CTGGACGCGCGGCGGGAGGGCGAGC    27

RESULT 10
HUMCALPAIL/c
LOCUS       HUMCALPAIL           609 bp    mRNA        linear    PRI 31-DEC-1994
DEFINITION  Human calpactin 1 light chain mRNA, complete cds.
ACCESSION   M81457
VERSION     M81457.1  GI:179874
KEYWORDS    calpactin I light chain.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 609)
  AUTHORS   Dooley,T.P., Weiland,K.L. and Simon,M.
  TITLE     cDNA sequence of human pII calpactin I light chain
  JOURNAL   Genomics 13 (3), 866-868 (1992)
  MEDLINE   92347895
  PUBMED    1386341
COMMENT     Original source text: Homo sapiens (tissue library: lambda gt11)
            cDNA to mRNA.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="presumed at 1q21"
                     /cell_type="primary keratinocyte"
                     /tissue_lib="lambda gt11"
     gene            1..609
                     /gene="calpactin 1 light chain"
     CDS             72..365
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Left column (RESULT 12)

ORIGIN
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                    /mol_type="genomic DNA"
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Query Match        46.5%;  Score 557;  DB 6;  Length 579;
Best Local Similarity  99.7%;  Pred. No. 2.9e-108;
Matches 579;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy    1 GGAACTAAAAAAGAGAACTTTATTTATTGAGGGGATGCAAGGGACCAAACAATACAAAAAATCAA   60
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Db  579 GGAACTAAAAAAGAGAACTTTATTTATTGAGGGGATGCAAGGGACCAAACAATACAAAAAATCAA  520

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCTGCTTGTGTCAAATGAGAGTTAGATTTTATT  120
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Db  519 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCTGCTTGTGTCAAATGAGAGTTAGATTTTATT  460

Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGTGGGGAAGCTGTGGG  180
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Db  459 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGTGGGGAAGCTGTGGG  400

Qy  181 GCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  240
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Db  399 GCAGATTCCTTAAGCGACCCCTTT-GAACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  341

Qy  241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  300
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Db  340 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  281

Qy  301 GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  360
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Db  280 GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  221

Qy  361 TCCAGGTTCCTTCATTATTTTGTCCACGCCAGAGAGCTCTTTTTGATTTTCCAAAAATCCA  420
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Db  220 TCCAGGTTCCTTCATTATTTTGTCCACGCCAGAGAGCTCTTTTTGATTTTCCAAAAATCCA  161

Qy  421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  480
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Db  160 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  101

Qy  481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATT  540
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Db  100 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATT   41

Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGGCGCGGAC  581
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Db   40 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGGCGCGGAC    1
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RESULT 12
AX396675
LOCUS       AX396675                 571 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 890 from Patent WO0212328.
ACCESSION   AX396675
VERSION     AX396675.1  GI:21067422
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   King,G.E., Meagher,M.J., Xu,J. and Secrist,H.
  TITLE     Compositions and methods for the therapy and diagnosis of colon
            cancer
  JOURNAL   Patent: WO 0212328-A 890 14-FEB-2002;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..571
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ORIGIN
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Right column (RESULT 13)

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Best Local Similarity  98.7%;  Pred. No. 5.2e-104;
Matches 537;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    1 GGAACTAAAAAAGAGAACTTTATTTATTGAGGGCAAGGGACCAAACAATACAAAAAATCAA   60
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Db   28 GNAACTAAAAAAANAACTTTATTTATTGAGGGCAAGGGACCAAACAATACAAAAAATCAA   87

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCTGCTTGTGTCAAATGAGAGTTAGATTTATT  120
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Db   88 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCTGCTTGTGTCAAATGAGAGTTANATTTTATT  147

Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG  180
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Db  148 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG  207

Qy  181 GCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  240
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Db  208 GCANATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  267

Qy  241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  268 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  327

Qy  301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  360
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Db  328 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTNTACACTGG  387

Qy  361 TCCAGGTTCCTTCATTATTTTGTCCAGCCAGAGAGGTCTTTTTGATTTTCCAAAAATCCA  420
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Db  388 TCCAGGTTCCTTCATTATTTTGTCCAGCCAGAGCCAGAGGTCTTTTTGATTTTCCAAAAATCCA  447

Qy  421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  448 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  507

Qy  481 GCGAATTTGTGAAATGGCATTCCATTTGAGATGGCATT  540
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Db  508 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGANATGGCATT  567

Qy  541 TTGG  544
        ||||
Db  568 TTGG  571
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RESULT 13
AY179865/c
LOCUS       AY179865                 646 bp    mRNA    linear   PRI 18-JAN-2003
DEFINITION  Macaca mulatta S100 calcium binding protein A10 (S100A10) mRNA,
            complete cds.
ACCESSION   AY179865
VERSION     AY179865.1  GI:27802540
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Sun,X.-Y., Tan,Y.-F., Qin,L., Bai,S.-X., Li,F.-X., Qiu,W.,
            Piao,Y.-S. and Wang,Y.-L.
  TITLE     Molecular cloning of genes critical to embryo implantation from
            Rhesus monkey by suppression subtractive hybridization
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 646)
  AUTHORS   Sun,X.-Y., Tan,Y.-F., Qin,L., Bai,S.-X., Li,F.-X., Qiu,W.,
            Piao,Y.-S. and Wang,Y.-L.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) State Key Laboratory of Reproductive
            Biology, Institute of Zoology, Chinese Academy of Science, Bei Si
            Huan Xi Lu, #25, Hai Dian District, Beijing 100080, China
FEATURES             Location/Qualifiers
     source          1..646
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RESULT 14 (AX899035/c)

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                              /protein_id="AAO21200.1"
                              /db_xref="GI:27802541"
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Query Match             44.2%;  Score 530;  DB 9;  Length 646;
Best Local Similarity   96.4%;  Pred. No. 1.7e-102;
Matches  542;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy      1 GGAACTAAAAAAGAAGAACTTATTATTGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db    617 GGAACTAAAAAAGAAGAACTTATTATTGCAAGGGGATGCAAACAATACAAAAATCAA 558

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db    557 AAGCTTATCTGGTATTTAACTTTCCTTTCTCTGCTTGTCAAATGGGAGTTAGATTTTTATT 498

Qy    121 TTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGGAAGCTGTGGG 180
          |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    497 TTTACATTGCTAAGGGTCCTGATCTGCTCATGAAATCCTTCATGGGGGGAAGCTGTGGG 438

Qy    181 GCAGATTCCTTAAGCGACCCTTGGGACAACTTCTTATCAGGGAGGAGCGAACTGCTCATT 240
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Db    437 GCAGATTCCTCAAGCGACCCTTGGGACAGCTCTTGTCAGGGAGGAGGGAAGCTGTCGTT 378

Qy    241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 300
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Db    377 TTTGCCTACTTCTTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 318

Qy    301 GTGAGGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
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Db    317 GTGAGGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTGCCATCTCTGCACTGG 258

Qy    361 TCCAGGTCCTTCATTATTTGTCCACAGCCCAGAGAGGGTCTTTTTGATTTCCAAAAATCCA 420
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Db    257 TCCAGGTCCTTCATTATTTGTCCACGGCCAGAGGGGTCTTTTTGATTTCCAAAAATCCA 198

Qy    421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 480
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Db    197 GGAAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCC 138

Qy    481 GCGAATTGTGAAAATGTAAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
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Db    137 GCGAATTGTGAAAATGTAAAACATCATGTTTCCATGGGGATGCGTCCATTTGAGACGGCATT 78

Qy    541 TTGGTGTGGTCCGTTGAAGCCT 562
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Db     77 TTGGTGTGGTCGTGTTGAAGCTT 56
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RESULT 14
AX899035/c
LOCUS       AX899035                582 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 14898 from Patent EP1033401.
ACCESSION   AX899035
VERSION     AX899035.1  GI:40053948
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
```

RESULT 15 (BD034568/c)

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              TITLE           Expressed sequence tags and encoded human proteins
              JOURNAL         Patent: EP 1033401-A 14898 06-SEP-2000;
                              Genset (FR)
              FEATURES        Location/Qualifiers
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Query Match             43.6%;  Score 523;  DB 6;  Length 582;
Best Local Similarity   97.9%;  Pred. No. 5.1e-101;
Matches  547;  Conservative    4;  Mismatches    4;  Indels    4;  Gaps    2;

Qy     30 GGAAGGGGATGCAAACATACAAAAATCAAAAGCTTATCTGTATTAACTTTCTTC 89
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Db    582 GGCAAGGGGATGCAAACATACAAAAATCAAAAGCTTATCTGTATTTAACTTTTCTTTC 523

Qy     90 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCTAAGTGTCCTGATCTGCT 149
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Db    522 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTTACATTTGCTAAGTGTCCTGATCTGCT 463

Qy    150 CATGAAATCCTTCTATGGGGGAAGCTGTGGGGCCAGATTCCTTAAGCGAGTTCCTTGGGACA 209
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Db    462 CATGAAATCCTTCTATGGGGGAAGCTGTGGGGCCAGATTCCTTAAGCGAGTTCC--GACA 405

Qy    210 ACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTTCTTCCCTTCTGCTTCAT 269
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Db    404 ACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTTCTTCCCTTCTGCTTCAT 345

Qy    270 GTGTACTACAAAATAGTCATTGCATGCAATGTGAGCCCGCAATAGGGGAAAAGAAGCT 329
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Db    344 GTGTACTACAAAATAGTCATTGCATGCAATGTGAGCCCGCAATAGGGGAAAAGAAGCT 285

Qy    330 CTGGAAGCCCACTTGCCATCTCACACTGGTCCTGGTTCCAGTCAGTTTGTCCACAGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 CTGGAAGCCCACTTGCCATCTCACACTGGTCCTGGTTCCAGTCAGTTTGTCCACAGC 225

Qy    390 CAGAGGGGTCTTTTTGATTTCCAAAATCCAGGGAACTCCTTTTCCATCTCTCAG 449
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Db    224 CAGAGGGTC--TTTGATTTCCAAAATCCAGGGAACTCCTTTTCCATCTCTCAG 167

Qy    450 GTCCTCCTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGAAAATGTAAACATCATGT 509
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Db    166 GTCCTCCTTGTTAAGTAGCCTTTATCCCCAGCGAATTGYGAAATGTAMACRTCATGT 107

Qy    510 TTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCCGA 569
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    106 TTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCCGA 47

Qy    570 GGGCGGCGGACGCTGGGC 588
          ||||||||||||| |||||
Db     46 GGCGGCGGCGGGGCTGTGCCC 28
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RESULT 15
BD034568/c
LOCUS       BD034568                582 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD034568
VERSION     BD034568.1  GI:22576310
KEYWORDS    JP 2001269182-A/10814.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 582)
  AUTHORS   Edwards,J.B.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 10814 02-OCT-2001;
            GENSET
COMMENT     OS  Homo sapiens (human)
            PN  JP 2001269182-A/10814
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PD   02-OCT-2001
PF   24-FEB-2000 JP 2000118773
PR   26-FEB-1999 US   60/122487
PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI   JORDAN
PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
     C12N5/10,
PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N5/00,C12N5/00, PC
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FH   Key         Location/Qualifiers.
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ORIGIN

Query Match        43.6%;  Score 523;  DB 6;  Length 582;
Best Local Similarity  97.9%;  Pred. No. 5.1e-101;
Matches 547;  Conservative 4;  Mismatches 4;  Indels 4;  Gaps 2;

Qy   30  GGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTTATCTGGTATTTAACTTTTCTTTC  89
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Db  582  GGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTTATCTGGTATTTAACTTTTCTTTC  523

Qy   90  TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTTACATTGCTAAGTGTCCTGATCTGCT 149
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Db  522  TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTTACATTGCTAAGTGTCCTGATCTGCT 463

Qy  150  CATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATTCCTTAAGCGACCCTTTGGGACA 209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||
Db  462  CATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATTCCTTAAGCGACCCTTT--GACA 405

Qy  210  ACTCTTATCAGGAGGAGGAACTGCTCATTGTCATTGTACTGTACTACAAAAATAGTCAT 269
         |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db  404  ACTCTTATCAGGAGGAGGAACTGCTCATTGTCATTGTACTGTACTACAAAAATAGTCAT 345

Qy  270  GTGTACTACAAAAATAGTCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCT 329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  344  GTGTACTACAAAAATAGTCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCT 285

Qy  330  CTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTTGTCCACAGC 389
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Qy  390  CAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAG 449
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  224  CAGAGGGTC--TTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAG 167

Qy  450  GTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGAAATGTAAACATCATGGT 509
         |||||||||||||||||||||||||:|||:||:||||||||||||||||||||:|||||||
Db  166  GTCCTCCTTTGTTAAGTAGCCTTTATYCCCAGCGAATTTGYGAAATGTAAACATCAMRTCATGGT 107

Qy  510  TTCCATGGCGTGTTCCATTTGAGATGGCATTTGGTGTGGTTCCGGTCCGTTGAAGCCTTGGCCGA 569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  106  TTCCATGGCGTGTTCCATTTGAGATGGCATTTGGTGTGGTTCCGGTCCGTTGAAGCCTTGGCCGA 47

Qy  570  GGCGCGGCGGACGCTGGGC 588
         ||||||||||| |||| ||
Db   46  GGCGCGGCGGGCGTGCGC 28

RESULT 16
CQ702692/c
LOCUS       CQ702692                538 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 47618 from Patent WO02070737.
ACCESSION   CQ702692
VERSION     CQ702692.1  GI:44263461
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
AUTHORS     Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE       Compositions and methods relating to osteoarthritis
JOURNAL     Patent: WO 02070737-A 47618 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES             Location/Qualifiers
     source          1..538
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match        43.0%;  Score 516;  DB 6;  Length 538;
Best Local Similarity  98.9%;  Pred. No. 1.6e-99;
Matches 530;  Conservative 0;  Mismatches 5;  Indels 1;  Gaps 1;

Qy    8  AAAAAGAACTTTATTTATTTGATGGCAGGGGATGCAAGGGGATGCAACAATACAAGAAAAATCAAAAGCTTA  67
         |||||||||| ||||||||||| |||||||||||||||||||||||||| || |||  |||||||||||||||
Db  535  AAAAAGAACCTTTATTTATTTGAGGGCAAGGGGATGCAAGGGGATGCAACCAATCCAAAAAATCAAAAGCTTA 476

Qy   68  TCTGGTATTTAACTTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTTTACAT 127
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  475  TCTGGTATTTAACTTTTCTTTCTCGCTCGTCAAATGAGAGTTAGATTTTATTTTTTACAT 416

Qy  128  TTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATT 187
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  415  TTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATT 356

Qy  188  CCTTAAGCGACCCTTTGGGCAACTCCTTATCAGGAGGAGGAACTGCTCATTTCTGCCT 247
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  355  CCTTAAGCGACCCTTTGGGCAACTCCTTATCAGGAGGAGGAACTGCTCATTTCTGCCT 296

Qy  248  ACTTCTTTCCCTTCTGCTTCATTGTACTACAAAAATAGTCATTGCATGCAATGGTGAGGC 307
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  295  ACTTCTTTCCCTTCTGCTTCATTGTACTACAAAAATAGTCATTGCATGCAATGGTGAGGC 236

Qy  308  CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  235  CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT 176

Qy  368  CCTTCATTATTTTGTCCACAGCCAGAGGGGTCTTTTGATTTTCCAAAAATCCAGGGAACT 427
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  175  CCTTCATTATTTTGTCCACAGCCAGAGGGGTCTTTTGATTTTCCAAAAATCCAGGGAACT 116

Qy  428  CCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATT 487
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  115  CCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATT 56

Qy  488  TGTGAAATGTAAACATCATGGTTTCCATTGGAGATGGCATTTTG 543
         |||||||||||||||||||||                       
Db   55  TGTGAAATGTAAACATCATGG-AACCATGGCGTGTTCCATTTGAGATGGCATTTTG 1

RESULT 17
AX616317/c
LOCUS       AX616317               2016 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 1 from Patent WO02094864.
ACCESSION   AX616317
VERSION     AX616317.1  GI:28447361
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Bejanin,S. and Tanaka,H.
TITLE       Human cdnas and proteins and uses thereof
JOURNAL     Patent: WO 02094864-A 1 28-NOV-2002;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1..2016
                     /organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

FEATURES   Location/Qualifiers
  source   1..482
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
ORIGIN

Query Match   39.3%; Score 471.6; DB 6; Length 482;
Best Local Similarity   99.2%; Pred. No. 4.5e-90;
Matches   474; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 GGAACTAAAAAGAACTTATTTATTGAGGGCAGGGATGCAAACATACAAAAATCAA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   478 GAACTAAAAAGAACTTATTTATTGAGGGCAGGGTGCAAACATACAAAAATCAA 419

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTGCTTCTGCTTGCTCAAATGAGAGTTAGATTTTATT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   418 AAGCTTATCTGGTATTTAACTTTCTTTCTTTCTGCTTCTGCTTGCTCAAATGAGAGTTAGATTTTATT 359

Qy   121 TTTACATTTGCTAAGTGCCTGATCTGCTTCATCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   358 TTTACATTTGCTAAGTGCCTGATCTGCTTCATCATGAAATCCTTCATGGGGGAAGCTGTGGG 299

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGGAGGAGCGAACTGCTCATT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGGAGGAGCGAACTGCTCATT 239

Qy   241 TCTGCCTACTTCTTTCCCTTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 TCTGCCTACTTCTTTCCCTTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 179

Qy   301 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 119

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 59

Qy   421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCTCCTCCTTGTAAGTAGCCTTTATCCC 478
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 GGGAACTCCTTTCCATGAGTACTCTCAGGTCTCCTCCTTGTAAGTAGCCTTTATCCC 1

RESULT 19
CQ713004/c
LOCUS   CQ713004   472 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION   Sequence 57930 from Patent WO02070737.
ACCESSION   CQ713004
VERSION   CQ713004.1 GI:42273861
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE   Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 57930 12-SEP-2002;
             Chondrogene Inc. (CA)
FEATURES   Location/Qualifiers
  source   1..472
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
ORIGIN

Query Match   38.5%; Score 461.4; DB 6; Length 472;
Best Local Similarity   98.7%; Pred. No. 6.8e-88;
Matches   465; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   73 TATTTAACTTTCTTTCTTTCTGCTTCTGCTTGCTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 132
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
5'UTR   1..1434
CDS   1435..1839
          /note="unnamed protein product"
          /codon_start=1
          /protein_id="CAD67623.1"
          /db_xref="GI:28447362"
          /translation="MAACQLLEITTFLRETFSCLPRPRTEPLVASTDHTKMPSQMEH
          AMETMMFTHKFAGDKGYLTKEDLRVLMKEFPGFPLENQKDPLAVDKIMKDLDQCRDG
          KVGFQSFFSLJAGLTIACNDYFVSHMKQKGKK"
3'UTR   1837..2016
polyA_signal 1965..1970
polyA_site   2001..2016
ORIGIN

Query Match   40.5%; Score 485.2; DB 6; Length 2016;
Best Local Similarity   94.7%; Pred. No. 6.7e-93;
Matches   502; Conservative   0; Mismatches   28; Indels   0; Gaps   0;

Qy   73 TATTTAACTTTCTTTCTTTCTGCTTCTGCTTGCTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 132
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2012 TTTTTTTTTTCTTTCTCTGCTTCTGCTTGCTCAAATGAGAGTTAGATTTTATTTTTACATTTGCT 1953

Qy   133 AAGTGCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCGTGTGGGGCAGATTCCTTA 192
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1952 AAGTGCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCGTGTGGGGCAGATTCCTTA 1893

Qy   193 AGCGACCCTTTGGGACAACTCTTATCAGGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 252
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1892 AGCGACCCTTTGGGACAACTCTTATCAGGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 1833

Qy   253 TTTCCCTTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGGCCGCA 312
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1832 TTTCCCTTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGGTGAGGGCCGCA 1773

Qy   313 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGGTCCAGGTCCTTC 372
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1772 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGGTCCAGGTCCTTC 1713

Qy   373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCAGGGAACTCCTTT 432
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1712 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 1653

Qy   433 TCCATGAGTACTCTCAGGTCCCCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 492
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1652 TCCATGAGTACTCTCAGGTCCCCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 1593

Qy   493 AATGTAAACATCATGGTTCCATGGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 552
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1592 AATGTAAACATCATGGTTCCATGGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 1533

Qy   553 GTTGAAGCCTTGGCCGAGGCCGCGGCCGCGGACGCTGGGCGCAGCT 602
            ||||||| || ||| |||
Db   1532 GTTGAAGCCACCAGAGGCTCAGTGCGCGAGGGTCGGGCAGGCAAGAAAAGGT 1483

RESULT 18
CQ701466/c
LOCUS   CQ701466   482 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION   Sequence 46392 from Patent WO02070737.
ACCESSION   CQ701466
VERSION   CQ701466.1 GI:42262233
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE   Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 46392 12-SEP-2002;
             Chondrogene Inc. (CA)

Qy 472 TATTTAACTTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTTATTTTTACATTTGCT 413
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 133 AAGTGTCCTGATCTGCTCATGAAAATCCTTCATGGGGAAGCTGTGGGCAGATTCCTTA 192

Db 412 AAGTGTCCTGATCTGCTCATGAAAATCCTTCATGGGGAAGCTGTGGGCAGATTCCTTA 353

Qy 193 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 352 AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTC 293

Qy 253 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 292 TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA 233

Qy 313 ATTAGGGAAAAGAAGCTCGGAAGCCCACTTGCCATCTCACACTGGTCCAGGTCCTTC 372
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 232 ATTAGGGAAAAGAAGCTCTGAAGCCCACTTGCCATCTCACACTGGTCCAGGTCCTTC 173

Qy 373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTTCCAAAAATCCAGGGAACTCCTTT 432
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 172 GTTATTTTGTCCACACGCCAGAGGGTCTTTTTGATTTTTCCAAAAATCCAGGGAACTCCTTT 113

Qy 433 TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 492
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 112 TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGTGA 53

Qy 493 AATGTAAACATCATGGTTTCCATGGGCGTGTTCCATTGAGATGGCATTTTG 543
         |||||||||||||||||||||||||| |||
Db 52   AATGTAAACATCATGTTTTCCATGTTTCCATGGGCGTGTTCCATTTGAGAGGCATTTTGG 2

RESULT 20
CQ704196/c
LOCUS   CQ704196   480 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION Sequence 49122 from Patent WO02070737.
ACCESSION   CQ704196
VERSION   CQ704196.1 GI:42264965
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE   Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 49122 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES   Location/Qualifiers
     source   1..480
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   37.4%; Score 448; DB 6; Length 480;
Best Local Similarity   95.8%; Pred. No. 4.9e-85;
Matches 460; Conservative   0; Mismatches 20; Indels 0; Gaps 0;

Qy   3 AACTAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAA 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 480 ACCTAAAAAGAACCTTTATTTATTGAGGGCAAGGGATGCAACCAATCCAAAAATCAAAA 421

Qy   63 GCTTATCTGGGTATTTAACTTTTCTTTCTCTGCTTGTCTCATGAAATCCTTCATGAGAGTTAGATTTTTATTTT 122
         |||||||||||||||||||||||| ||||||||||||||||||||
Db 420 GCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCTCATGAAATCCTTCATGAGAGTTAGATTTTTATTTT 361

Qy 123 TACATTTGCTAAGTGTCCTGATCTGCTCTCATGAAATCCTTATCAGGGAGCGAACTGCTCATTTC 182
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 360 TACATTTGCTAAGTGTCCTGATCTGCTCTCATGAAATCCTTATCAGGGAGCGAACTGCTCATTTC 301

Qy 183 AGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTC 242
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 300 AGATTCCTTAAGCGACCCTTTGGGCAACTCTTATCAGGGAGGAGCGAACTGCTCATTTC 241

Qy 243 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGGT 302
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTGTTCATGTACAAAATAGTCATGCATGCAATGGT 181

Qy 303 GAGGCCCGCAATTAGGGAAAAGAAGCTCTGAGAAGCCCACTTGCCATCTCTCACACTGGTC 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180 GAGGCCCGCAATTAGGGAAAAACAAGCTCTGGAAGCCCACTTGCCATCTCTCACACTGGTC 121

Qy 363 CAGGTCCTTCATTATTTTGTCCACAGCCAGCAGCCAGAGGGTCTTTTCCAAAAATCCAGG 422
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 120 CAGGTCCTTCATTATTTTGTCCACAGCCAGCAGCCAGAGGGTCTTTTGATTTTTCCAAAAATCCAGG 61

Qy 423 GAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC 482
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 GAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTTTCCCCAGC 1

RESULT 21
CQ711110/c
LOCUS   CQ711110   474 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION Sequence 56036 from Patent WO02070737.
ACCESSION   CQ711110
VERSION   CQ711110.1 GI:42271967
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE   Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 56036 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES   Location/Qualifiers
     source   1..474
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   37.2%; Score 446.4; DB 6; Length 474;
Best Local Similarity   98.9%; Pred. No. 1.1e-84;
Matches 469; Conservative   0; Mismatches   3; Indels 2; Gaps 2;

Qy   9 AAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAAT-ACAAAAATCAAAAGCTTA 67
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db 474 AAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAACAACNACCNCAAAAATCAAAAGCTTA 415

Qy   68 TCTGGTATTTAACTTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTTATTTTTACAT 127
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 414 TCTGGTATTTAACTTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTTATTTTTACAT 355

Qy 128 TTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGCAGATT 187
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 354 TTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGCAGATT 295

Qy 188 CCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCT 247
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 294 CCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCT 235

Qy 248 ACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGGTGAGGC 307
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 234 AATTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGGTGAGGC 175

Qy 308 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTCACACTGGTCCAGGT 367
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 174 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTCACACTGGTCCAGGT 115

Qy 368 CCTTCATTATTTTGTCCACAGCCAGCAGCCAGAGGGTCTTTTGATTTTTCCAAAAATCCAGGGAACT 427
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 114 CCTTCATTATTTTGTCCACAGCCAGCAGCCAGAGGGTCTTTTTGATTTTTCCAAAAATCCAGGGAACT 55

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Qy   428 CCTTTTCCATGAGTACTCTCAGGTCC-TCCTTTGTTAAGTAGCCTTTATCCCCA 480
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    54 CCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 1
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RESULT 22
CQ711578/c
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LOCUS       CQ711578                448 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 56504 from Patent WO02070737.
ACCESSION   CQ711578
VERSION     CQ711578.1  GI:42272435
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE     Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 56504 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES             Location/Qualifiers
     source          1..448
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match             36.2%;  Score 434.4;  DB 6;  Length 448;
  Best Local Similarity 99.6%;  Pred. No. 3.9e-82;
  Matches  446;  Conservative    0;  Mismatches   1;  Indels   1;  Gaps   1;
```

```
Qy     1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAAC-AATACAAAAATCA 59
         ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   448 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAAATACAAAAATCA 389

Qy    60 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTAT 119
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTAT 329

Qy   120 TTTTACATTTGCTAAGTGTCCTGATCGTCCTGATCCTCTATGGGGGAAGCTGTGG 179
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 TTTTACATTTGCTAAGTGTCCTGATCGTCCTGATCCTCTATGGGGGAAGCTGTGG 269

Qy   180 GGCAGATTCCTTAAGCGACACCCTTGGGACAACCTTATCAGGGAGGACGGACTGCTCAT 239
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 GGCAGATTCCTTAAGCGACACCCTTGGGACAACCTTATCAGGGAGGACGGACTGCTCAT 209

Qy   240 TTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT 299
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 TTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT 149

Qy   300 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCAGAGGGTCTTTTGCCATCTCTACACTG 359
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCAGAGGGTCTTTTGCCATCTCTACACTG 89

Qy   360 GTCCAGGTCCTTCATTATTTGTCCAGGCCAGAGGGTCTTTTGATTTTCCAAAAATCC 419
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88 GTCCAGGTCCTTCATTATTTGTCCAGGCCAGAGGGTCTTTTGATTTTCCAAAAAACC 29

Qy   420 AGGGAACTCCTTTCCATGAGTACTCTC 447
         |||||||||||||||||||||||||||
Db    28 AGGGAACTCCTTTCCATGAGTACTCTC 1
```

RESULT 23
BOVCALPI/c
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LOCUS       BOVCALPI                604 bp    mRNA    linear   MAM 26-APR-1993
DEFINITION  Bovine calpactin I light chain (p11) mRNA, complete cds.
ACCESSION   M16464 J02779
VERSION     M16464.1  GI:162784
KEYWORDS    calpactin I light chain; protein kinase; tyrosine kinase.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 604)
  AUTHORS   Saris,C.J., Kristensen,T., D'Eustachio,P., Hicks,L.J., Noonan,D.J.,
            Hunter,T. and Tack,B.F.
  TITLE     cDNA sequence and tissue distribution of the mRNA for bovine and
            murine p11, the S100-related light chain of the protein-tyrosine
            kinase substrate p36 (calpactin I)
  JOURNAL   J. Biol. Chem. 262 (22), 10663-10671 (1987)
  MEDLINE   87280130
   PUBMED   3038891
COMMENT     Original source text: Bovine intestine epithelial cell, cDNA to
            mRNA.
            Draft entry and printed copy of sequence for [1] kindly provided by
            B.F.Tack, 20-JUL-1987.
            Polyadenylation signals are located at positions 481-486, 525-530
            and 578-583.
FEATURES             Location/Qualifiers
     source          1..604
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
     mRNA            1..604
                     /product="calpactin I lc mRNA"
     CDS             64..357
                     /note="calpactin I light chain"
                     /codon_start=1
                     /protein_id="AAA30423.1"
                     /db_xref="GI:162785"
                     /translation="MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLE
                     NQKDPLAVDKIMKDLDQCRDCKVGFQSFFSLIAGLTIACNDYFVVHMKQKGKK"
ORIGIN      86 bp upstream of NcoI site.
```

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Query Match             36.2%;  Score 434;  DB 4;  Length 604;
  Best Local Similarity 88.6%;  Pred. No. 4.8e-82;
  Matches  505;  Conservative    0;  Mismatches  60;  Indels   5;  Gaps   3;
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```
Qy     2 GAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAA 61
         |||||||||||||||  ||||||||||| ||||         |     ||||||||||||
Db   602 GAACTAAAAAGAACTTGTTTATTGAGGGCAAGGCAAGCAAGGAAGCAAGCAATATAAAAAATCAAA 543

Qy    62 AGCTTATCTGG---TATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTA 118
         |||||||||||   || |||| ||||||||||||||| | |||| || ||||| |||||||
Db   542 AGCTTATCTGGCTTTTAATTGACTTTCTTTCTTCTGCTTCTCAAAATGGAGTTGGATTTTA 483

Qy   119 TTTTACATTTGCTAAGTGTCCTGATCGTCCTGATCCTCTATGGGGGAAGCTGTG 178
         ||| ||||||| |||  |||||   |||| ||  |     | |  ||||||||||
Db   482 TTTGTACATTTTCTATGGGTCC--CATATGCTCA-GAAATCCTTATACAGGGAAGCTGTG 425

Qy   179 GGGCAGATTCCTTAAGCGACACCCTTGGGACAACCTTATCAGGGAGGAGCGAACTGCTCA 238
         || |||| ||||||| |||  ||| |   || | |||||||||| || |  |||||||||
Db   424 GGACAGAGTCCTTAAGTGACCCCTTTATCGAGAATTCTTATCAGGGTGGGAGTAATTGCTCA 365

Qy   239 TTTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAA 298
         ||  ||||||||||||||| |||||||||||||||||||||||| |||||||||||| ||
Db   364 ATGCTGCCTACTTCTTTCCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGGA 305

Qy   299 TGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCAGAGGGTCTTTTGCCATCTCTACACT 358
         |||||||| ||  | ||||| ||||||||||||||||||||||||||||||||||| ||| | ||||
Db   304 TGGTGAGCCCAGCGATTAGCGAAAAGAAGCTCTGGAAGCCCAGAGGGTCTTTTGCCGTCTCGACACT 245

Qy   359 GGTCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTCCTTTTTGATTTTTCCAAAAATC 418
         ||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||
Db   244 GGTCCAGGTCCTTCATTATTTGTCCACGCCAGAGGGTCTTTTTGATTTTTCCAAAAATC 185

Qy   419 CAGGGAACTCCTTTCCATGAGTACTCCCTTTGTTAAGTAGCCTTTATCCC 478
         ||||||||||||||||||||||||||  ||||||||||||| ||||||| |
Db   184 CAGGGAACTCCTTTCCATGAGTACTCCAGGTCTTCCAGGTCTTCCTTTGTTAAGTAACCTTTATCAC 125

Qy   479 CAGCGAATTGTGAAATGTAAACATCATCGTTTTCCATTGAGATGGCA 538
         | ||||||||||||||||||||| ||||||
Db
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Db   124 CTGCAAATTTGTGAAATGTGAACATCATGGTTTCCATGGCGTCGTCTCCATTGAGACGGCA 65

Qy   539 TTTTGGTGTGTCGTTGAAGCCTTCGCCG 568
          ||| ||| |||||||| |||||||||||
Db   64 TTTTGGTGAAGTCTCGTTGAAACCCTTGGCGG 35

RESULT 24
AX777886/c
LOCUS   AX777886   434 bp   DNA   linear   PAT 14-JUL-2003
DEFINITION   Sequence 43 from Patent WO03039443.
ACCESSION   AX777886
VERSION   AX777886.1 GI:32694880
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
             Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
TITLE   Novel genetic markers for leukemias
JOURNAL   Patent: WO 03039443-A 43 15-MAY-2003;
             Deutsches Krebsforschungszentrum (DE) ;
             Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
             PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES   Location/Qualifiers
     source   1..434
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   35.3%;   Score 423;   DB 6;   Length 434;
Best Local Similarity 99.8%;   Pred. No. 1e-79;
Matches   434;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

Qy   126 ATTTGCTAAGTGTCCTGATCTGCTCATGAGAATCCTCTATGGGGAAGTGTGGGCAGA 185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 ATTTGCTAAGTGTCCTGATCTGCTCATGAGAATCCTCTATGGGGAAGTGTGGGCAGA 375

Qy   186 TTCCTTAAGGCACCCTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGC 245
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   374 TTCCTTAAGGCACCCTTT -GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGC 316

Qy   246 CTACTTCTTTCCCTTCGCTTCAGTGTACTACAAAAATAGTCATTGCAATGGTGAG 305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315 CTACTTCTTTCCCTTCGCTTCAGTGTACTACAAAAATAGTCATTGCAATGGTGAG 256

Qy   306 GCCCCGCAATTAGGGAAAAGAGAGCTCTGGAGCCCACTTTGCCATCTCTACACTGGTTCCAG 365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 GCCCCGCAATTAGGGAAAAGAGAGCTCTGGAGCCCACTTTGCCATCTCTACACTGGTTCCAG 196

Qy   366 GTCCTTCATTATTTTGTCCAGCGCAGAGGGTCTTTTGATTTCCAAAAATCAGGGAA 425
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   195 GTCCTTCATTATTTTGTCCACGACGAGGGTCTTTTGATTTCCAAAAATCAGGGAA 136

Qy   426 CTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTTGTTAAGTAGCCTTTATCCCCAGCGAA 485
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 CTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTTGTTAAGTAGCCTTTATCCCCAGCGAA 76

Qy   486 TTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATTTTGGT 545
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   75 TTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATTTTGGT 16

Qy   546 GTGGTTCCGTTGAAGC 560
          ||||||||||||||||
Db   15 GTGGTTCCGTTGAAGC 1

RESULT 25
HUMP11A/c
, LOCUS   HUMP11A   480 bp   DNA   linear   PRI 07-JAN-1995

DEFINITION   Human p11 protein gene sequence.
ACCESSION   M77483
VERSION   M77483.1 GI:189420
KEYWORDS   p11 protein.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 480)
AUTHORS   Harder,T., Kube,E. and Gerke,V.
TITLE   Cloning and characterization of the human gene encoding p11:
             structural similarity to other members of the S-100 gene family
JOURNAL   Gene 113 (2), 269-274 (1992)
MEDLINE   92241679
PUBMED   1533380
COMMENT   Original source text: Homo sapiens (tissue library: lambda-FixII)
             DNA.
FEATURES   Location/Qualifiers
     source   1..480
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /cell_type="fibroblast"
                     /tissue_lib="lambda-FixII"
     gene   92..402
                     /gene="p11"
     misc_feature   92..100
                     /gene="p11"
                     /note="beta-DRE element"
     GC_signal   176..183
                     /gene="p11"
     GC_signal   196..203
                     /gene="p11"
     misc_feature   214..223
                     /gene="p11"
                     /note="beta-DRE element"
     GC_signal   220..227
                     /gene="p11"
     GC_signal   395..402
                     /gene="p11"
ORIGIN

Query Match   32.5%;   Score 389.2;   DB 9;   Length 480;
Best Local Similarity 94.6%;   Pred. No. 1.7e-72;
Matches   439;   Conservative   0;   Mismatches   13;   Indels   12;   Gaps   3;

Qy   560 CCTTGGCCGAGGCGGCGGCGGACGGCTGGGCGAGCTGGGCGAGC-------- TGGACGCGG 610
          |||||||||||||||||||||||||||||||||||||||| |||||||||
Db   461 CCTTGGCCGAGGCGGCGGCGGACGGCTGGGCGAGCTGGGCGAGCGACGTGGGCGACGTGGGCGACGCGG 402

Qy   611 GGCGGAGAGGCGGCGGAGCGGCGGCGGGCGGCGCTGTGGCGGAGGAGCGCTCGGCGGGCGCTCCCCAGC 670
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 GGCGGAGAGGCGGCGGAGCGGCGGCGGGCGGCGCTGTGGCGGAGGAGCGCTCGGCGGGCGCTCCCCAGC 342

Qy   671 AGGGAGGCGCGGGGAGGCGGGAGAGCGGCCTGGGGAGGAGCCTCGGCGGGCGCTCCCCAGC 730
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 AGGGAGGCGGTGCGGAGCGGGAGAGCGGCGGAGGAGCGGCCTCGGCGGGCGCTCCCCAGC 282

Qy   731 CCTGTCTCCTCCCCTTCTGCCCGCCGCTCCCCGGCGACTCCCCGGCGCCCCCGCCGCCGCGC 790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 CCTGTCTCCTCCCCTTCTGCCCGCCGCTCCCCGGCGACTCCCCGGCGCCCCCGCCGCCGCGC 222

Qy   791 CCTGCCCCTCGCTCCCCGGGACCCCGCCTCGCAGAGGCATCCCCACCC 850
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 CCTGCCCCTCGCTCCCCGGGACCCCGCCTCGCAGAGGCATCCCCACCC 162

Qy   851 TGTAAACTTCTCTTCAGTAGAAACGGTCCTGCTCTCCAATATTTCAGGGCATCCCCACCC 910
          |||||||||||||||||||||||||||| ||||||||| |||||||||||||||||
Db   161 TGTAAACTTCTCTTCAGTAGAAACGGTCCTGCTCTCGAATATTT -AGGGCATCCCCACCC 104

Qy   911 TGAGCCTGCCCTTCCTTCCTCCGGGTTTGGTTTTAGAAAGTGTACAAATCAAAGAAACCCGGCC 970
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   103 TGAGCCTGCCCTTCCTTCCTCCGGGTTTGGTTTTTAGAAAGTGTACAAATCAAAGAAACCCGGCC 44

```
Qy    971  GTCCTGCGGGTGGGCACGCTCGGCGCAGAACCAGAGTAACCGG 1014
           |||||||||||||||||||||||||||||||||||||||||||
Db     43  GTCCTGCGGGTGGGCACG-TGGCGCAGAACCAGAGTAACCGG 1

RESULT 26
CQ700639/c
LOCUS       CQ700639              392 bp    DNA      linear     PAT 03-FEB-2004
DEFINITION  Sequence 45565 from Patent WO02070737.
ACCESSION   CQ700639
VERSION     CQ700639.1  GI:42261406
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE       Compositions and methods relating to osteoarthritis
JOURNAL     Patent: WO 02070737-A 45565 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES             Location/Qualifiers
     source          1..392
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             31.5%;  Score 377.4; DB 6; Length 392;
Best Local Similarity   99.5%;  Pred. No. 5.4e-70;
Matches   389;  Conservative    0;  Mismatches    1;  Indels   1;  Gaps   1;

Qy      1  GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391  GAAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 332

Qy     61  AAGCTTATCTCGTATTAACTTTCTTCTTCCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331  AAGCTTATCTCGTATTAACTTTCTTCTTCCTCGCTTGTCAAATGAGAGTTAGATTTTATT 272

Qy    121  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGT-GG 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    271  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTCGG 212

Qy    180  GGCAGATTCCTTAAGGCGACCCCTTGGGACAACAACTCTTATCAGGGAGGAGCAACTGCTCAT 239
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211  GGCAGATTCCTTAAGGCGACCCCTTGGGACAACAACTCTTATCAGGGAGGAGCAACTGCTCAT 152

Qy    240  TTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151  TTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT 92

Qy    300  GGTGAGCGCCCGCAATTAGGAGAAAAGAAGCTCGGAGCCCCACTTTGCCATCTCTACACTG 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91  GGTGAGCGCCCGCAATTAGGAGAAAAGAAGCTCGGAGCCCCACTTTGCCATCTCTACACTG 32

Qy    360  GTCCAGGTCCTTCATTATTTGTCCACAGCC 390
           |||||||||||||||||||||||||||||||
Db     31  GTCCAGGTCCTTCATTATTTGTCCACAGCC 1

RESULT 27
AB098817
LOCUS       AB098817              534 bp    mRNA     linear     MAM 12-APR-2003
DEFINITION  Bos taurus mRNA for similar to calpactin I light chain, partial
            cds, clone: ORCS13327.
ACCESSION   AB098817
VERSION     AB098817.1  GI:28189323
KEYWORDS
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

```
REFERENCE   1
AUTHORS     Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.,
            Takahashi,T., Imai,K., Hirasawa,A., Shiojima,S., Ikawa,H.,
            Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.
TITLE       Characterization of gene expression profiles in early bovine
            pregnancy using a custom cDNA microarray
JOURNAL     Mol. Reprod. Dev. 65 (1), 9-18 (2003)
MEDLINE     22544902
PUBMED      12658628
REFERENCE   2  (bases 1 to 534)
AUTHORS     Tsujimoto,G., Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V.,
            Nakano,H., Konno,T., Ushizawa,K., Takahashi,T., Imai,K.,
            Hirasawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Izaike,Y.,
            Todoroki,J. and Hashizume,K.
TITLE       Direct Submission
JOURNAL     Submitted (25-DEC-2002) Gozoh Tsujimoto, National Research
            Institute for Child Health and Development, Department of
            Molecular, Cell Pharmacology; 3-35-31 Taishido, Setagaya, Tokyo
            154-8567, Japan (E-mail:gtsujimoto@nch.go.jp, Tel:81-3-3149-2476,
            Fax:81-3-3149-1252)
COMMENT     This work was performed to collaborate with Developmental Biology
            Department, National Institute of Agrobiological Sciences. Address:
            2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan.  Phone & Fax:
            81-29-838-8633  e-mail: kazuha@affrc.go.jp
            This work was funded by Organized Research Combination System
            (ORCS) project of Ministry of Education, Culture, Sports, Science
            and Technology.
FEATURES             Location/Qualifiers
     source          1..534
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="ORCS13327"
                     /clone_lib="ORCS bovine utero-placenta cDNA"
                     /dev_stage="adult"
                     /note="mixture of uterus and placenta"
     CDS             complement(<246. .>476)
                     /codon_start=1
                     /product="similar to calpactin I light chain"
                     /protein_id="BAC56353.1"
                     /db_xref="GI:28189324"
                     /translation="GDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRD
                     GKVGFQSFFSLIAGLTIACNDYFVHMKQKGKK"
ORIGIN
         3' end partial sequence.

Query Match             31.2%;  Score 374.2; DB 4; Length 534;
Best Local Similarity   86.0%;  Pred. No. 2.7e-69;
Matches   461;  Conservative    0;  Mismatches   69;  Indels   6;  Gaps   4;

Qy      5  CTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGC 64
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      1  CTNTAAAGGAATAAGTTTATTGAGAGCAAGAGGATGCAAGCAATATAAAAATCAAAAGC 60

Qy     65  TTATCTGG---TATTTAACTTTCTTTCTTCCTCGTTGTCAAATGAGAGTTAGATTTTATTT 121
           ||||||||   |||  |||||||||| ||||| || ||||||||| ||||||| ||||||
Db     61  TTATCTGGCTTAATGAACTTTTCTTTTCCTCCTTCTCAAATGAGAGTTGGATTTTATTT 120

Qy    122  TTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGTGGGG 181
           |||||||||||||| |||||| |||||||||||| || |||||||| ||||||||||||||
Db    121  GTACATTTTCTATGGGTCC--CATATGCTCA-GAAATCCTTATACAGGGGAAGCTGTCGGGA 178

Qy    182  CAGATTCCTTAAGCGACCCTTTGGGACAACTTCTTATCAGGGAGGAGCAACTGCTCATT 241
           ||||||||||||| |||||| ||||||||||| |||||||||||||||||||||||||||
Db    179  CAGAGTCCTTAAGTGACCCTTTATGAGAATTCTTATCAGGGGTGGGAGTAATTGCTCAATG 238

Qy    242  CTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGG 301
           |||||||||||||||||||| ||||||||||| |||||||| |||||||||||||||
Db    239  CTGCCTACTTCTTTCCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCGATGG 298

Qy    302  TGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGAGAGTCTCGAAGCCCACTTTGCCATCTCTACACTGGT 361
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BC025044/c
LOCUS           BC025044                604 bp    mRNA    linear   ROD 29-JUN-2004
DEFINITION      Mus musculus S100 calcium binding protein A10 (calpactin) mRNA
                (cDNA clone MGC:36182 IMAGE:4949465), complete cds.
ACCESSION       BC025044
VERSION         BC025044.1  GI:19263549
KEYWORDS        MGC.
SOURCE          Mus musculus (house mouse)
  ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE       1  (bases 1 to 604)
  AUTHORS       Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
                Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
                Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
                Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
                Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
                Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
                Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
                Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
                Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
                McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
                Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
                Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
                Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
                Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
                Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
                Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
                Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
                Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE         Generation and initial analysis of more than 15,000 full-length
                human and mouse cDNA sequences
  JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED       12477932
REFERENCE       2  (bases 1 to 604)
  AUTHORS       Strausberg,R.
  TITLE         Direct Submission
  JOURNAL       Submitted (05-MAR-2002) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
REMARK          NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT         Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Jeffrey Green M.D.
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Baylor College of Medicine Human Genome
                Sequencing Center
                Center code: BCM-HGSC
                Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                Contact: amg@bcm.tmc.edu
                Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
                Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                A.N., Gibbs, R.A.
                Clone distribution: MGC clone distribution information can be found
                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                Series: IRAK Plate: 60 Row: g Column: 24
                This clone was selected for full length sequencing because it
                passed the following selection criteria: matched mRNA gi: 6677832.
FEATURES             Location/Qualifiers
     source          1..604
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                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="MGC:36182 IMAGE:4949465"
                     /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating
                     ductal carcinoma. 5 month old virgin mouse."
                     /clone_lib="NCI_CGAP_Mam6"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
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Db      299  ||||   ||| |||   |||||||||||||||||||||||||||  |||||   |||||||||  358
             TGAGCCAGCGATTAGCGAAAAGAAGCTCTGGAAGCCCACTTGCCGTCTCGACACTGGT
Qy      362  CCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAG  421
             |||||||||||||||||||||||||   |||||| |||||   ||||||||||||||||
Db      359  CCAGGTCCTTCATTATTTGTCCACGGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAG  418
Qy      422  GGAACTCCTTTTCCATGAGTACTCCTCCAGGTCCTCCTTTGTAAGTAGCCTTTATC-CCCA  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      419  GGAACTCCTTTTCCATGAGTACTCCTCCAGGTCCTCCTTTGTAAGTAAGCCTTTATCACCTG  478
Qy      481  GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTGAGATGATGG  536
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||  ||
Db      479  GCAAATTTGTGAAATGTGAACATCATGGGTTTCCATGGCGTGCCCCATTGAGACGCGG  534
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RESULT 28
CQ709131/c
LOCUS           CQ709131                384 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION      Sequence 54057 from Patent WO02070737.
ACCESSION       CQ709131
VERSION         CQ709131.1  GI:42269942
KEYWORDS        .
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
  AUTHORS       Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE         Compositions and methods relating to osteoarthritis
  JOURNAL       Patent: WO 02070737-A 54057 12-SEP-2002;
                Chondrogene Inc. (CA)
FEATURES             Location/Qualifiers
     source          1..384
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match             30.3%;  Score 363.6;  DB 6;  Length 384;
Best Local Similarity   98.7%;  Pred. No. 4.7e-67;
Matches  366;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Qy        8  AAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTTA  67
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      378  AAAAAAGACTTTATTTATTGAGGGCAAGGGGATGCAACCAATCCAAAAATCAAAAGCTTA  319
Qy       68  TCTGGTATTTAACTTTCTTCTTCTCTGCTTGTCAAATGAGAGTGATTTTATTTTTACAT  127
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      318  TCTGGTATTTAACTTTCTTCTTCTCTGCTTGTCAAATGAGAGTGATTTTATTTTTACAT  259
Qy      128  TTGCTAAGTGTCCTGATCGTCCTCATGAAATCCTTCATGGGGGAAGCTGTGGGGCAGATT  187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      258  TTGCTAAGTGTCCTGATCGTCCTCATGAAATCCTTCATGGGGGAAGCTGTGGGGCAGATT  199
Qy      188  CCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTCTGCCT  247
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      198  CCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTCTGCCT  139
Qy      248  ACTTCTTCCCTTCCGCTTCATGTGCTTACTACAAAATAGTCAATGGCAATGGTGAGGC  307
             ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      138  ACTTCTTCCCTTCCGCTTCATGTNCTACAAAATAGTCAATGGCAATGGTGAGGC  79
Qy      308  CCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACTTGCCATCTCACACTGGTCCAGGT  367
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       78  CCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACTTGCCATCTCCACACTGGTCCAGGT  19
Qy      368  CCTTCATTATT  378
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Db       18  CCTTCATTATT  8
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RESULT 29

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REFERENCE    1
AUTHORS      Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE        Compositions and methods relating to osteoarthritis
JOURNAL      Patent: WO 02070737-A 51172 12-SEP-2002;
             Chondrogene Inc. (CA)
FEATURES     Location/Qualifiers
  source     1..365
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
ORIGIN

Query Match     28.8%;  Score 344.8;  DB 6;  Length 365;
Best Local Similarity   98.4%;  Pred. No. 4.8e-63;
Matches  358;  Conservative    0;  Mismatches   4;  Indels   2;  Gaps   1;

Qy      1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    362 GGAACTAAAAAGAACTTATTTATTGAGG--CAAGGGATGCAAACAATACAAAAATCAA 305

Qy     61 AAGCTTATCTGGTATTAACTTTCTTTCTTCTTGTCAAATGAGAGTTAGATTTTATT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTTGTCAAATGAGAGTTAGATTTTATT 245

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 185

Qy    181 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 GCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT 125

Qy    241 TCTGCCTACTTCTTTCCCTTCGTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 TCTGCCTACTTCTTTCCCTTCGTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 65

Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 5

Qy    361 TCCA 364
            ||||
Db      4 TCCA 1
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RESULT 31
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LOCUS        AX306168/c
DEFINITION   AX306168
ACCESSION    Sequence 919 from Patent WO0188188.
VERSION      AX306168
KEYWORDS     AX306168.1   GI:17645451
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1
AUTHORS      Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
TITLE        Method for examining ischemic conditions
JOURNAL      Patent: WO 0188188-A 919 22-NOV-2001;
             School Juridical Person Nihon University (JP)
FEATURES     Location/Qualifiers
  source     1..600
             /organism="Mus musculus"
             /mol_type="unassigned DNA"
             /db_xref="taxon:10090"
ORIGIN

Query Match     28.7%;  Score 343.6;  DB 6;  Length 600;
Best Local Similarity   79.6%;  Pred. No. 9.2e-63;
Matches  476;  Conservative    0;  Mismatches  99;  Indels  23;  Gaps  5;

Qy      7 AAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTT 66
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             /note="synonym: p11"
             /db_xref="LocusID:20194"
             /db_xref="MGI:1339468"
CDS          47..340
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             /codon_start=1
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             /db_xref="GI:1926350"
             /db_xref="LocusID:20194"
             /db_xref="MGI:1339468"
             /translation="MPSQMEHAMETMMLTFHRFAGDKDHLTKEDLRVLMEREFPGFLE
             NQKDPLAVDKIMKDLDQCRDGKVGFQSFLSVAGLTIACNDYFVVNMKQKGKK"
ORIGIN

Query Match     29.1%;  Score 348.8;  DB 10;  Length 604;
Best Local Similarity   80.3%;  Pred. No. 7.1e-64;
Matches  466;  Conservative    0;  Mismatches  92;  Indels  22;  Gaps  4;

Qy      7 AAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTT 66
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    570 AAAAAAGAACTTTCTTTATTGAGGGCAATGGGATGCAAACAATATAAAACTCAGAAGCTT 511

Qy     67 ATCTGGTAT----TTAACTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTTT 122
            ||||||||      ||||||||||||||||||||||||||||||||||||||||| ||||
Db    510 CTCTGCCATTGGATTAAGTTTTCTCTCTCAGATTGTTGAGTTGGAGTTGGATCTCATTTG 451

Qy    123 TACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGTG 182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    450 CACATTTCCTAAGGGTCCTGATCTGCTCACAA---------GAAGCAGTGGGGC 406

Qy    183 AGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGGCGGA--ACTGCTCATT 240
            ||||||||||||||||||||||||||||||||  ||||| ||||||
Db    405 AGATTCCTCAAGTGACCCCCGTGGTGACAACGCACCAGGGGTACCAGTGCTCCAG 346

Qy    241 TCTGCCTACTTCTTTCCCTTCGTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
            || ||||||||| |||||| ||| ||||||||||||||||||||||||||
Db    345 TTGGCCTATTTCTTTCCCCTTCTGCTTCATGTTTCATTGTTTACTACAAAAATAGTCATTGCATGCCAATG 286

Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
            || |||||||||||||||||||||||||||||||||||||||||||||||
Db    285 GTGAGGCCCGCCACTAGTGATGAGAAAGCTCTGGAAGCCCACTTTGCCATCTCGGCACTGG 226

Qy    361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGGTCTCTTTTGATTTTCCAAAAATCCA 420
            ||||||||||||||||||||||||||||||||||| ||||||| |||||||||
Db    225 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGATCCCAGAGATTTTCCAAAAACCCA 166

Qy    421 GGGAACTCCTTTCCATGAGTACTCCAGGTCTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
            ||||||||||||||||||||||||||||||||||||||||||||
Db    165 GGGAACTCCCGTTCCATGAGCACTCTCAGGTCTCCTCCTTTGTTCAAGTGGTCTTTGTCGCCT 106

Qy    481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGATGCGTGTTCCATTTGAGATGGCATT 540
            ||||||| ||||||||| ||||||||||||||||||
Db    105 GCAAACCTGTGAAACGTAAGCATCATGGTTTCCATGGCGTGCTCCATTTGGGATGGCATT 46

Qy    541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCGCGGAGGA 580
            || |||| |||||  ||||||  |||| |||||
Db     45 TTGAAG-AGTCGTGCGAAACCTGGGCCCCCGGAGGCGCAGCA 7
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RESULT 30
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LOCUS        CQ706246/c
DEFINITION   CQ706246
ACCESSION    Sequence 51172 from Patent WO02070737.
VERSION      CQ706246
KEYWORDS     CQ706246.1   GI:42267015
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDS            /product="calpactin I lc mRNA"
               69. .362
               /note="calpactin I light chain"
               /codon_start=1
               /protein_id="AAA37363.1"
               /db_xref="GI:309134"
               /translation="MPSQMSHAMETMMLTFHRFAGDKDHLTKEDLRVLMEREFPGFLE
               NQKDPLAVDKIMKDLDQCRDGKVFQSFLSLVAGLTIACNDYFVVNMKQKGKK"

ORIGIN         91 bp upstream of NcoI site; chromosome 3.

Query Match    28.7%;    Score 343.6;  DB 10;    Length 600;
Best Local Similarity   79.6%;    Pred. No. 9.2e-63;
Matches  476;    Conservative   0;  Mismatches  99;    Indels  23;    Gaps    5;

Qy        7  AAAAAGAAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTT   66
             ||||||||| |||| |||| ||||||||||||||||| ||| | || ||||| ||||||
Db      591  AAAAAGGACTTTCTTTATTGAGGGCAATGGCATGGATGCAAACAATATAAAACTCAGAAGCTT  532

Qy       67  ATCTGGTAT----TTAACTTTCTTTCTCTGCTTGTCTGTCAAATGAGAGTTAGATTTTATTTT  122
             ||||||||    |||  |||||| |||||||||||||| ||| | |||||||||||||||||
Db      531  CTCTGCCATTGGATTAAGTTTCTTCTCTCTCAGATTGTTGAATTGGAGTTGGATCTCATTTG   472

Qy      123  TACATTTGCTAAGTGTCCTGATCTGTCTCATGAAAATCCTTCTATGGGGGAAGCTGTGGGGC  182
             |||||||||||||||||| |||||||||||||||| |||||||||           |||||||
Db      471  CACATTTCCTAAGGGTCCTGATCTGCTCACAA-----------GAAGCAGTGGGGC  427

Qy      183  AGATTCCTTAAGCGACCCCTTTGG-GACAACTCTTATCAGGAGGAGGAGGCGAACTGCTCATTT  241
             ||||||||| | |||| ||| ||| ||||||||| |||  ||| |  |||
Db      426  AGATTCCTCAAGTGACCCCGTGGTGAACACGCACCACCAGGGTGGGGTACCAGTGCTCCAGT   367

Qy      242  CTGCCTACTCTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGG  301
             |||||| |||||||||||||||||||  |||||||||||||||||||||||||||||||
Db      366  TGGCCTATTTCTTCCCTCTGCTTCATGTTTACTACAAAATAGTCATTGCATGCAATGG   307

Qy      302  TGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGT  361
             ||||||||||| |||| ||| || ||||||||||  ||| ||||| |||||  |||||||
Db      306  TGAGCCCATTTGCCCTTCCCCTCTGCCTGTTCCATTTGAGATGCCATTT  247

Qy      362  CCAGGTCCTTCATTATTGTTGTCCAGCAGAGGGTCTTTTGAATTTCCAAAAAATCCAG  421
             |||||||||||||||||||||||||||||||||||||| || |||||||||| ||||||
Db      246  CCAGGTCCTTCATTATTTTTGTCCAGCAGAGGATCCTTTGAGAAAAGCTCTGGAAGAAAGCTCTGATAGAAAAGCTCTGGAAGCCCACTTTGCCATCTCGCCACTGGT  187

Qy      422  GGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCAG  481
             |||||||||||||||||||||||||||||||| ||||||| ||||||| |||| |||
Db      186  GGAACTCCCGTTCCATGAGCACTCTCAGGTCCTCCTTGTTCAAGTGGTCTTTGTCGCCTG  127

Qy      482  CGAATTGTGAAATGTAAACATCATCATGTTTCCATGGCGTGTTCCATTTGAGATGGCATTT  541
             ||| |||||||| || ||||| |||| |||| || |||| |||  |||| | || ||||||
Db      126  CAAACCTGTGAAACGTAAGCATCATCATGTTTCCATGGCGTGCTCCATTTGGGATGGCATTT   67

Qy      542  TGGTGTGGTCCGTTGAAGCCTTGG--CCGAGGCGCGGCGACGCTGGGCGAGCTGGGC  597
             |||||||||||||||||||||| ||  ||||||||||||||||||||||||||||||
Db       66  TGAAG-AGTCTGTCGAAACCTGGGCCCCGAAGCGCAGCAGTCCTTGAAGAGCTGGGC   10

RESULT 33
CQ711127/c
LOCUS       CQ711127                407 bp    DNA        linear    PAT 03-FEB-2004
DEFINITION  Sequence 56053 from Patent WO02070737.
ACCESSION   CQ711127
VERSION     CQ711127.1  GI:42271984
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE     Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 56053 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .407
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Db      591  AAAAAGGACTTTCTTTATTGAGGGCAATGGCATGGATGCAAACAATATAAAACTCAGAAGCTT  532
Qy       67  ATCTGGTAT----TTAACTTTCTTTCTCTGCTTGTCTGTCAAATGAGAGTTAGATTTTATTTT  122
Db      531  CTCTGCCATTGGATTAAGTTTCTTCTCTCTCAGATTGTTGAATTGGAGTTGGATCTCATTTG   472
Qy      123  TACATTTGCTAAGTGTCCTGATCTGTCTCATGAAAATCCTTCTATGGGGGAAGCTGTGGGGC  182
Db      471  CACATTTCCTAAGGGTCCTGATCTGCTCACAA-----------GAAGCAGTGGGGC  427
Qy      183  AGATTCCTTAAGCGACCCCTTTGG-GACAACTCTTATCAGGAGGAGGAGGCGAACTGCTCATTT  241
Db      426  AGATTCCTCAAGTGACCCCGTGGTGAACACGCACCACCAGGGTGGGGTACCAGTGCTCCAGT   367
Qy      242  CTGCCTACTCTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGG  301
Db      366  TGGCCTATTTCTTCCCTCTGCTTCATGTTTACTACAAAATAGTCATTGCATGCAATGG   307
Qy      302  TGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGT  361
Db      306  TGAGCCCATTTGCCCTTCCCCTCTGCCTGTTCCATTTGAGATGCCATTT  247
Qy      362  CCAGGTCCTTCATTATTGTTGTCCAGCAGAGGGTCTTTTGAATTTCCAAAAAATCCAG  421
Db      246  CCAGGTCCTTCATTATTTTTGTCCAGCAGAGGATCCTTTGAGAAAAGCTCTGGAAGAAAGCTCTGATAGAAAAGCTCTGGAAGCCCACTTTGCCATCTCGCCACTGGT  187
Qy      422  GGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCAG  481
Db      186  GGAACTCCCGTTCCATGAGCACTCTCAGGTCCTCCTTGTTCAAGTGGTCTTTGTCGCCTG  127
Qy      482  CGAATTGTGAAATGTAAACATCATCATGTTTCCATGGCGTGTTCCATTTGAGATGGCATTT  541
Db      126  CAAACCTGTGAAACGTAAGCATCATCATGTTTCCATGGCGTGCTCCATTTGGGATGGCATTT   67
Qy      542  TGGTGTGGTCCGTTGAAGCCTTGG--CCGAGGCGCGGCGACGCTGGGCGAGCTGGGC  597
Db       66  TGAAG-AGTCTGTCGAAACCTGGGCCCCGAAGCGCAGCAGTCCTTGAAGAGCTGGGC   10

RESULT 32
MUSCALPI/c
LOCUS       MUSCALPI                600 bp    mRNA        linear    ROD 12-JUN-1993
DEFINITION  Mouse calpactin I light chain (p11) mRNA, complete cds.
ACCESSION   M16465 J02779
VERSION     M16465.1  GI:192360
KEYWORDS    calpactin I light chain; protein kinase; tyrosine kinase.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Saris,C.J., Kristensen,T., D'Eustachio,P., Hicks,L.J., Noonan,D.J.,
            Hunter,T. and Tack,B.F.
  TITLE     cDNA sequence and tissue distribution of the mRNA for bovine and
            murine p11, the S100-related light chain of the protein-tyrosine
            kinase substrate p36 (calpactin I)
  JOURNAL   J. Biol. Chem. 262 (22), 10663-10671 (1987)
MEDLINE     87280130
PUBMED      3038891
COMMENT     Original source text: Mouse fibroblast (ANN-1), cDNA to mRNA.
            Draft entry and clean copy sequence for [1] kindly provided by
            B.F.Tack, 20-JUL-1987.
            Calpactin I light chain mRNA levels are low in liver, heart and
            testes, moderate in brain, spleen and thymus, and high in kidney,
            intestine and lung.  A polyadenylation signal is located at
            positions 572-577.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
     mRNA            1. .600
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Qy    293  ATGCAATGGTGAGGCCCGCAATTAGGAAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTC  352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219  ATGCAATGGTGAGGCCCGCAATTAGGAAAAAGAAGCTCGGAAGCCCACTTTGCCATCTC  160

Qy    353  TACACTCGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCA  412
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159  TACACTCGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCA  100

Qy    413  AAAATCCAGGGAACTCCTTTCCATGAGTACTCTCAGTTCCTCCTTTGTTAAGTAGCCTT  472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     99  AAAATCCAGGGAACTCCTTTCCATGAGTACTCTCAGTTCCTCCTTTGTTAAGTAGCCTT   40

Qy    473  TATCCCCAGCGAATTGTGAAATGTAAACATCATGGTTT  511
           ||||||||||||||||||||||||||||||||||||||
Db     39  TATCCCCAGCGAATTGTGAAATGTAAACATCATGGTTT    1

RESULT 35
AC005921
LOCUS       AC005921               164679 bp    DNA     linear   PRI 03-JUN-1999
DEFINITION  Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.
ACCESSION   AC005921
VERSION     AC005921.3  GI:4982556
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 164679)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone hRPK.294_J_22
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 164679)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boutwell,C.,
            Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., Corliss,D., Depayre,E., Devon,K., Dewar,K.,
            Donelan,L., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R.,
            Gage,D., Gardyna,S., Geraigery,K., Grant,G., Hagos,B., Heaford,A.,
            Herena,L., Horton,L., Howland,J.C., Jacotot,L., Jones,C., Kann,L.,
            Karatas,A., Lehoczky,J., Macdonald,P., Marquis,N., McEwan,N.,
            McGurk,A., McKernan,K., Meldrim,J., Molla,M., Morris,W., Morrow,J.,
            Mychaleckyj,J., Nahf,R., Naylor,J., Niloff,M., O'Connor,T.,
            O'Donnell,P., Pavlin,B., Peterson,K., Riley,R., Roberts,D., Roy,A.,
            Severy,P., Stange-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C.,
            Subramanian,A., Tesfaye,S., Tichovolsky,N., Torruella-Miller,I.,
            Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,Y., Wyman,D.,
            Ye,W.J., Zhao,J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 164679)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
            Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K.,
            Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
            Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
            Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,
            Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
            Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
            Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
            Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
            Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
            Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-FEB-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 164679)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
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ORIGIN
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match          28.6%;  Score 343; DB 6;  Length 407;
Best Local Similarity   98.7%;  Pred. No. 1.2e-62;
Matches  377;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    3;

Qy      3  AACTAAAAAGAACTTATTATTGAGGGCAAGGGATGCAAAC--AATACAAAAATCAA   60
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Db    407  AACTAAAAAGAACTTATTATTGAGGGCAAGGGATGCAAACCAAATACAAAAATCAA  348

Qy     61  AAGCTTATCTGGTATTAACTTTCTTTCTCTGCTTCTCTCATGAAATCCTTCTCA  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    347  AAGCTTATCTGGTATTAACTTTCTTTCTCTGCTTGTCTCATGAAATGAGATTTATT  288

Qy    121  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG  228

Qy    181  GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGCGACTGCTCATT  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    227  GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGCGACTGCTCATT  168

Qy    241  TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    167  TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  108

Qy    301  GTGAGGGCCGCAATTAGG-AAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTG  359
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    107  GTGAGGGCCGCAATTAGGGAAAAGAAGAGCTCGGAAGCCCACTTTGCCATCTCTACACTG   48

Qy    360  GTCCA-GGTCCTTCATTATTTT  380
           ||||| ||||||||||||||
Db     47  GTCCAGGGTCCTTCATTANTTT   26

RESULT 34
CQ671113/c
LOCUS       CQ671113                 339 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 16039 from Patent WO02070737.
ACCESSION   CQ671113
VERSION     CQ671113.1  GI:42164059
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
  TITLE     Compositions and methods relating to osteoarthritis
  JOURNAL   Patent: WO 02070737-A 16039 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES             Location/Qualifiers
     source          1..339
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match          28.1%;  Score 337.4; DB 6;  Length 339;
Best Local Similarity   99.1%;  Pred. No. 1.8e-61;
Matches  338;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    173  GCTGTGGGGCAGATTCCTTAAGCGACCCTTTGGGACAACCCTTATCAGGAGGAGCGAAC  232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    339  GCTGTGGGGCAGATTCCTTAAGCGACCCTTTGGGACAACCCTTATCAGGAGGAGCGAAC  280

Qy    233  TGCTCATTTCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGC  292
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Db    279  TGCTCATTTCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGC  220
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             Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
             Cooke,P., DeAreliano,K., Depayre,E., Devon,K., Dewar,K.,
             Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
             Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
             Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
             Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,
             Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
             Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
             Naylor,J., Niloff,M., O'Connor,T., Riley,R., Roberts,D., Roy,A., Severy,P.,
             Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
             Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
             Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
             Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
  TITLE      Direct Submission
  JOURNAL    Submitted (13-APR-1999) Whitehead Institute/MIT Center for Genome
             Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   5  (bases 1 to 164679)
  AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
             Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
             Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
             Cooke,P., DeAreliano,K., Depayre,E., Devon,K., Dewar,K.,
             Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
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             Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,
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             Naylor,J., Niloff,M., O'Connor,T., Riley,R., Roberts,D., Roy,A., Severy,P.,
             Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
             Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
             Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
             Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
  TITLE      Direct Submission
  JOURNAL    Submitted (01-JUN-1999) Whitehead Institute/MIT Center for Genome
             Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jun 3, 1999 this sequence version replaced gi:4582484.
            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

            Only the last 164679 base pairs of this clone are being submitted.
            The remainder overlaps accession number AC004590 (WICGR project
            L314).
FEATURES             Location/Qualifiers
     source          1..164679
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /map="17"
                     /clone="hRPK.294_J_22"
                     /clone_lib="RPCI-11 human BAC library"
     repeat_region   44..190
                     /rpt_family="L2"
     repeat_region   complement(199..353)
                     /rpt_family="L2"
     repeat_region   354..645
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     repeat_region   1999..2143
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     repeat_region   2063..2209
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     repeat_region   complement(3018..3085)
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     repeat_region   complement(3209..3496)
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     repeat_region   complement(3506..3797)
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                     /rpt_family="L1MB2"
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                     /rpt_family="MSTC"
     repeat_region   complement(5119..5437)
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     repeat_region   complement(5651..5838)
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     repeat_region   5994..6301
                     /rpt_family="AluSx"
     repeat_region   7317..7495
                     /rpt_family="(TTTC)n"
     repeat_region   complement(7496..7777)
                     /rpt_family="AluSc"
     repeat_region   complement(7896..8002)
                     /rpt_family="L2"
     repeat_region   complement(8215..8513)
                     /rpt_family="AluSg"
     repeat_region   complement(8522..8576)
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     repeat_region   10158..10261
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     repeat_region   complement(10325..10597)
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     repeat_region   12057..12353
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     repeat_region   complement(12758..12815)
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     repeat_region   12816..12981
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     repeat_region   complement(13422..13798)
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     repeat_region   13828..14208
                     /rpt_family="L2"
     repeat_region   14209..14503
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     repeat_region   14504..15234
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     repeat_region   complement(18420..18615)
                     /rpt_family="MIR"
     repeat_region   18748..18848
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     repeat_region   19153..19186
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     repeat_region   19221..19264
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     repeat_region   19330..19620
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     repeat_region   21934..21979
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     repeat_region   22021..22141
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     repeat_region   22175..22333
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Query Match   27.6%;   Score 330.8;   DB 9;   Length 164679;
Best Local Similarity   75.6%;   Pred. No. 9.1e-60;
Matches 464;   Conservative   0;   Mismatches 142;   Indels   8;   Gaps   4;

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Qy        9 AAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTTAT      68
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Db   130543 AAAAAGGATGTGTCAATTGAGGCCAAGAGATGCAAACAATCCAAAGACCAAAAGCCTAT  130602

Qy       69 CTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTTACATT     128
            |||| ||||  |||||| ||||| |||||| |||||| ||||||| | | || |||||
Db   130603 TATTTAATTAAC-TTCCTTTCTTTGCTTGTTGTTAGATGAGATTTTGAGTTTGATGTGTCTGTT  130661

Qy      129 TGCTAAGTGTCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGGCAGATTC     188
            |  | ||||| |||||||||||| |||| |||  |||| ||||||||||||||||||
Db   130662 TTCT--TGGCCCTGGTCTGCTCATGAAAGCCTTCTACAGGGGGAAGCTGTGGGCAGGTTC  130719

Qy      189 CTTAAGCGACCCCTTGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTCTGCCTA     248
            |||  || ||  ||||||| ||| ||||| || ||||||| |  |   ||||| ||||
Db   130720 CTATAGCGACTCTTGGGAGAACTCTCACAGGGCTG--AGTAATTGCTTAGTTCTTGCCTG  130777

Qy      249 CTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTGTCATTGCATGCAATGGTGAGGCC     308
            |||||  || |||||||| ||||| ||||  |||||| ||||  | ||||||| ||||||
Db   130778 CTTCGTTTCCCTTCTGCTTCATAGGTACTACAAAAATAGTTGTTGTCCACAGTGGTGAGCCC  130837

Qy      309 CGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTCGGTCCAGGTC     368
            ||| ||||||| |||||||||||||||||||||| ||||||||||||| |||||||||||
Db   130838 CGCAGTGAGTGAAAACAAGTTCTGGAAGTTCTGGAAGTTCTGCCATCGCTGTGTTCCATGTC  130897

Qy      369 CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACTC     428
            ||||||| |||| ||||||||||||||||| ||| ||||||||||||||||||||||||
Db   130898 CTTCATTGTTATGTCTGCTGCACCCAGCCAGAGAGGGTCTTTTTGATTCTCCAAAAATCCAAGGAACTC  130957

Qy      429 CTTTTCCATGAGTACTCTCAGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT     488
            |||| ||||||| || ||||||||| || |||| |||||| || |||||||||||| ||
Db   130958 CTTTTCCCATGAGTACTTTCAGCCCTTTTATCCCGCCGGCAAATCT  131017

Qy      489 GTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGCTGTG     548
            || ||||||| |||| || |||||||| || |  |||||| ||| |||  |||| |||
Db   131018 GTGAAACGTAAACACACACGGTTTCCATGGTGTGTTCCATTGGACTGGGGTTGTTCGTGAG  131077

Qy      549 GTCCGGTTGAAGCCTTGGC---CGAGGCGCGGCGAGCGTGGGCGCAGCTGGGCGAGCTGGA     605
            ||||| ||||||| |||| |   ||| ||| ||| |||| ||||||||| |||
Db   131078 ATCGTGTTGAAAGCCTTGGCTGAGGTGCGTTGGGCGGCCGCTTGGCGCAGCTGGGCCTCAGGGC  131137

Qy      606 CGGGGGCGGAGAG     619
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Db   131138 CCCTCGGAACGAG  131151
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RESULT 36
CQ711784/c
LOCUS   CQ711784   330 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION   Sequence 56710 from Patent WO02070737.
ACCESSION   CQ711784
VERSION   CQ711784.1   GI:42272641
KEYWORDS   .
SOURCE   Homo sapiens (human)
    ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
   AUTHORS   Liew,C.C., Marshall,W.E. and Zhang,H.
   TITLE   Compositions and methods relating to osteoarthritis
   JOURNAL   Patent: WO 02070737-A 56710 12-SEP-2002;
            Chondrogene Inc. (CA)
FEATURES   Location/Qualifiers
     source   1..330
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
ORIGIN

Query Match   27.5%;   Score 330;   DB 6;   Length 330;
Best Local Similarity   100.0%;   Pred. No. 6.8e-60;
Matches 330;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy       99 CAAATGAGAGTTAGATTTTATTTTTACATTTGCTAAGTGTCCTGATCGTCGCTCATGAAATC     158
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      330 CAAATGAGAGTTAGATTTTATTTTTACATTTGCTAAGTGTCCTGATCGTCGCTCATGAAATC     271

Qy      159 CTTCTATGGGGAAGCTGTGGGGCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATC     218
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      270 CTTCTATGGGGAAGCTGTGGGGCAGATTCCTTAAGCGACCCTTGGGACAACTCTTATC     211

Qy      219 AGGGAGGAGGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTAC     278
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      210 AGGGAGGAGGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTAC     151

Qy      279 AAAATAGTCATTGCAATGGTGAGGCCCGCCAATTAGGGAAAAGAAGCTCTGGAAGCC     338
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      150 AAAATAGTCATTGCAATGGTGAGGCCCGCCAATTAGGGAAAAGAAGCTCTGGAAGCC      91

Qy      339 CACTTTGCCATCTCTACACTGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTC     398
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      399 TTTTTGATTTTCCAAAAATCCAGGGAACTC     428
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Db       30 TTTTTGATTTTCCAAAAATCCAGGGAACTC       1
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RESULT 37
BD251901/c
LOCUS   BD251901   600 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Potassium channel interactors and uses therefor.
ACCESSION   BD251901
VERSION   BD251901.1   GI:33061671
KEYWORDS   JP 2002530104-A/34.
SOURCE   Rattus sp.
    ORGANISM   Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1   (bases 1 to 600)
   AUTHORS   Rhodes,K., Betty,M., Ling,H.P. and An,W.
   TITLE   Potassium channel interactors and uses therefor
   JOURNAL   Patent: JP 2002530104-A 34 17-SEP-2002;
            MILLENNIUM PHARMACEUTICALS INC,AMERICAN HOME PRODUCTS CORP
COMMENT   OS   Rattus sp. (rat)
            PN   JP 2002530104-A/34
            PD   17-SEP-2002
            PF   19-NOV-1999 JP 2000583959
            PR   20-NOV-1998 US   60/109333,25-NOV-1998 US   60/110033 PR
            30-NOV-1998 US   60/110277,23-APR-1999 US   09/298731 PR
            09-JUL-1999 US   09/350614,09-JUL-1999 US   09/350874 PR
            21-SEP-1999 US   09/399913,21-SEP-1999 US   09/400492 PI
            KENNETH RHODES,MARIA BETTY,HUAI PING LING,WENQIAN AN PC
            C12N15/09,A61K31/711,A61K38/00,A61K45/00,A61P9/00,A61P25/00, PC
            A61P25/08,
            PC   A61P43/00,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC
            G01N33/53,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N5/00,A61K37/02 CC
            Potassium channel interactors and uses therefor FH   Key
            Location/Qualifiers   (52)...(336)
FEATURES   Location/Qualifiers
     source   1..600
                        /organism="Rattus sp."
                        /mol_type="genomic DNA"
                        /db_xref="taxon:10118"
     FT   CDS
ORIGIN

Query Match   27.5%;   Score 329.8;   DB 6;   Length 600;
Best Local Similarity   77.8%;   Pred. No. 8e-60;
Matches 458;   Conservative   0;   Mismatches 107;   Indels   24;   Gaps   4;

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Db    509  CTCTGTCATTGGATTAACTTTCTTTTCTTCTGTTGTCGAATTGGAGTTGGATGTGTTATTTG  450
           |||||||||||||||||| |||||||||||||||| |||||||||||||||||||||||
Qy    123  TACATTTGCTAAGTGTCCTGGTCCTGATCGTCATGAAATCCTTCATGGGGGGAAGCTGTGGGGC  182

Db    449  CACATTTCCTAAGGGTCCTGATCTGCTCA--------------CAGGAAGCAGTGGGGC  405
           ||||||||||||||||||||||||||
Qy    183  AGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGAGGAGCGAACTGCTCATTTC  242

Db    404  AGATTCCTCAGTTGACCCCATGGGAGGAGGACGCATCAAGGTGTGGGTACCAGGGC-----T  349

Qy    243  TGCCTACTTCTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGT  302
           ||||||||||||
Db    348  CCAGTTGGCCTACTTCTTCTGCTTCATGTGTCCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGAT  289

Qy    303  GAGGGCCCGCAATTAGGAGGAAAAGAAGCTCTGGAGCCCACTTTGCCCATCCTCCACTCGTC  362
           ||| |||  ||||||||||||||||||||||||||||||||||||||
Db    288  GAGCCCGCCACTAGTGATAGAAAGCTCTGGAAGCCCACTTTTCCATCTCCGGCACTGGTC  229

Qy    363  CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTCTCCTTTGTAAGTAGCCTTTATCCCCAGC  422
           ||||||||||||||||||||||||||||
Db    228  CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTTGTAAGTAGTAGTTTTTTCCCCTGC  169

Qy    423  GAACTCCTTTCCATGAGTACTCCCAGGTCCTCAGGTCGTGTTCCATTTGAGATGGCATTTT  482
           ||||||||||||||||||||||||||||||||
Db    168  GAACTCCCTTTCCATGAGCACTCTCAGGTCCTCCCTCAGTAGTTTTTTCCCCTGC  109

Qy    483  GAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTT  542
           ||||||||||||||||||||||
Db    108  AAACCTGTGAAATGTAAGCATCATGGTTTCCATGGGGATGGCATTTT  49

Qy    543  GGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGACGCGTGGGGCGAG  591
           |||||||||||||||||
Db    48   GAAG-AATCTGTGAAACCTGGGCCCTGAGGCGCTGAGTCTTTGGAAG  1
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RESULT 39
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AR473726/c
LOCUS       AR473726                600 bp    DNA         linear   PAT 20-FEB-2004
DEFINITION  Sequence 64 from patent US 6689581.
ACCESSION   AR473726
VERSION     AR473726.1  GI:42712140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Rhodes,K., Betty,M., Ling,H.-P. and An,W.
  TITLE     Potassium channel interactors and uses therefor
  JOURNAL   Patent: US 6689581-A 64 10-FEB-2004;
FEATURES             Location/Qualifiers
     source          1..600
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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Query Match             27.5%;  Score 329.8;  DB 6;  Length 600;
Best Local Similarity   77.8%;  Pred. No. 8e-60;
Matches    458;  Conservative    0;  Mismatches  107;  Indels  24;  Gaps  4;

Qy      7  AAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTT  66
           |||||  ||| |||||||||||||||||||||||| ||||||||||| |||||
Db    569  AAAAAAGAACTTTCTTTATTGAGGGCAACCGGATGCAAACAATATAAAACTCGAAAGCTC  510

Qy     67  ATCTGGTAT-----TTAACTTTCTTTTCTTCTGTTGTCGAATTGGAGTTGGATGTGTTATTTT  122
           ||||||||    |||| ||
Db    509  CTCTGTCATTGGATTAACTTTCTTTTCTTCTGTTGTCGAATTGGAGTTGGATGTGTTATTTTG  450

Qy    123  TACATTTGCTAAGTGTCCTGGTCCTGATCGTCATGAAATCCTTCATGGGGGGAAGCTGTGGGGC  182
           ||||||||||||||||||
Db    449  CACATTTCCTAAGGGTCCTGATCTGCTCA--------------CAGGAAGCAGTGGGGC  405

Qy    183  AGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGAGGAGCGAACTGCTCATTTC  242
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Db 404 AGATTCCTCAGTTGACCCCATGGGAGAGGACGGCATCAAGGTGTGGGTACCAGGGC----T 349

Qy 243 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGT 302
       |||| || |||||||||||||||||||||||||||||
Db 348 CCAGTTGGCCTACTTCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGAT 289

Qy 303 GAGGCCCGCAATTAGGAAAAGAAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 288 GAGCCCGCCACTAGTGATAGAAGCTCGGAAGCTCGGAAGCCCACTTTTCCATCTCGGCACTGGTC 229

Qy 363 CAGGTCCTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG 422
       |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 228 CAGGTCTTTCATTATTTTGTCCACAGCCAGAGGGTCCTTTTGATTTTCCAAAAACCCAGG 169

Qy 423 GAACTCCTTTCCATGAGTACTCTCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC 482
       |||||||||||||||||||||||||||||||||||| ||| |||||||||||||||
Db 168 GAACTCCCTTTCCATGAGCACTCTCAGTCCTCCTTTGTCAAGTAGTTTTTTTCCCCTGC 109

Qy 483 GAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTT 542
       |||||||||||||||||||||||||||||||||||||||||||||||||
Db 108 AAACCTGTGAAATGTAAGCATCATGGTTTCCATTTGGGATGGCATTTT 49

Qy 543 GGTGTGGTCCGTTGAAGCCTTGGCCGCAGGCCGCGGCGACGCTGGGCGAG 591
       | ||||| ||| ||| | ||| ||||||||||
Db 48 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCAGTCTTTGGAAG 1

RESULT 40
AX407293/c
LOCUS   AX407293   600 bp   DNA   linear   PAT 14-JUN-2002
DEFINITION Sequence 64 from Patent WO0226984.
ACCESSION   AX407293
VERSION   AX407293.1   GI:21440003
KEYWORDS
SOURCE   Rattus sp.
  ORGANISM   Rattus sp.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE   1
  AUTHORS   Rhodes,K., Betty,M., Ling,H.P. and An,W.
  TITLE   Potassium channel interactors and uses therefor
  JOURNAL   Patent: WO 0226984-A 64 04-APR-2002;
           Millennium Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..600
                     /organism="Rattus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10118"
     CDS   52..339
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD35214.1"
                     /db_xref="GI:21440004"
                     /translation="MPSQMEHAMETMMLTFHRFAGEKNYLTKEDLRVLMEREFPGFLE
                     NQKDPLAVDKIMKDLDQCRDGKVGFQSFLSLVAGLIIACNDYFVVHMKQKK"
ORIGIN

Query Match   27.5%;   Score 329.8; DB 6; Length 600;
Best Local Similarity   77.8%; Pred. No. 8e-60;
Matches 458;   Conservative   0; Mismatches 107; Indels   24; Gaps   4;

Qy   7 AAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTT 66
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Db 569 AAAAAAAGAACTTTCTTTTATTGAGGGCAACCGATGCAACAATATAAAACTCGAAAGCTC 510

Qy   67 ATCTGGTAT----TTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
       |||||||| |||| |||||| ||||||||||||||||||||||||||| |||
Db 509 CTCTGTCATTGGATTAACTTTTCTTTCTCTGCTTGTCGAATTGGAGTTGGATGTTATTTG 450

Qy 123 TACATTTGCTAAGTGTCCTAGAGTGTCCTGATCCTGCTTCATGAAATCCTTCATGGGGGAAGCTGTGGGGC 182
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 449 CACATTTCCTAAGGGTCCTGATCTGCTCA----------------CAGGAAGCAGTGGGGC 405

RESULT 41
AX401698/c
LOCUS   AX401698   573 bp   DNA   linear   PAT 06-JUN-2002
DEFINITION Sequence 1374 from Patent WO0210453.
ACCESSION   AX401698
VERSION   AX401698.1   GI:21337878
KEYWORDS
SOURCE   Rattus norvegicus (Norway rat)
  ORGANISM   Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE   1
  AUTHORS   Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and
           Elashoff,M.R.
  TITLE   Molecular toxicology modeling
  JOURNAL   Patent: WO 0210453-A 1374 07-FEB-2002;
           Gene Logic, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..573
                     /organism="Rattus norvegicus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10116"
                     /note="EMBL/GenBank Accession No. J03627"
ORIGIN

Query Match   27.5%;   Score 329.2; DB 6; Length 573;
Best Local Similarity   78.2%; Pred. No. 1.1e-59;
Matches 455;   Conservative   0; Mismatches 103; Indels   24; Gaps   4;

Qy   7 AAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTT 66
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 563 AAAAAAAGAACTTTCTTTTATTGAGGGCAACCGATGCAACAATATAAAACTCGAAAGTC 504

Qy   67 ATCTGGTAT----TTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
       |||||||| |||| |||||| ||||||||||||||||||||||||| |||
Db 503 CTCTGTCATTGGATTAACTTTTCTTTCTCTGCTTGTCGAATTGGAGTTGGATGTTATTTG 444

Qy 123 TACATTTGCTAAGTGTCCTAGAGTGTCCTGATCCTGCTTCATGAAATCCTTCATGGGGGAAGCTGTGGGGC 182
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 443 CACATTTCCTAAGGGTCCTAAGGGTCCTGATCGCTCA----------CAGGAAGCAGTGGGGC 399

Qy 183 AGATTCCTCAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGGCGAACTGTGCTCATTTC 242

Db   443 CACATTTCCTAAGGGTCCTGATCTGCTCA------------------CAGGAAGCAGTGGGGC 399

Qy   183 AGATTCCTAAGGCGACCCTTTGGGACAACTCCTTATCCAGGAGGAGGAGGAACTGCTCATTTC 242
         |||||||| |||| || |||| |||| ||||||||||||||||| |||||
Db   398 AGATTCCTCAGTTGCTTCCCTTCCCTTCGCTTCATGTGTACTACACAAAATAGTCATTGCAATGGT 398

Qy   398 AGATTCCTCAGTTGACCCCATGGGAGGAGGACGCATCAAGGTGTGGGTACCAGGGC----T 343
         ||||||||| ||| |||||||||| | || |||||||| ||| ||||
Db   243 TGCCTACTTCTTCTGCTTCCCTTCGCTTCATGTGTACTACACAAAATAGTCATTGCAATGGT 302

Qy   243 TGCCTACTTCTTCTGCTTCCCTTCGCTTCATGTGTACTACACAAAATAGTCATTGCAATGGT 302
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   342 CCAGTTGGCCTACTTCTTCTGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATGAT 283

Qy   342 CCAGTTGGCCTACTTCTTCTGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATGAT 283
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 GAGGCCCGCAATTAGGAGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362

Qy   303 GAGGCCCGCAATTAGGAGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   282 GAGCCCCGCCACTAGTGATAGAAAGCTCTGGAAGCCCACTTTTCCATCTCGGCACTGGTC 223

Qy   282 GAGCCCCGCCACTAGTGATAGAAAGCTCTGGAAGCCCACTTTTCCATCTCGGCACTGGTC 223
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 CAGGTCCTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG 422

Qy   363 CAGGTCCTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG 422
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   222 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 163

Qy   222 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 163
         |||||||| ||||||||||||||||||||||||||| |||||||||||||||| ||||
Db   423 GAACTCCTTTTCCATGAGTACTCTCAGGTCCCTTGTTAAGTAGCCTTTATCCCCAGC 482

Qy   423 GAACTCCTTTTCCATGAGTACTCTCAGGTCCCTTGTTAAGTAGCCTTTATCCCCAGC 482
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   162 GAACTCCCTTTCCATGAGCAGCACTCTCAGGTCCCTTGTCAAGTAGTTTTTTCCCCTGC 103

Qy   162 GAACTCCCTTTCCATGAGCAGCACTCTCAGGTCCCTTGTCAAGTAGTTTTTTCCCCTGC 103
         |||||||| |||||||||||||||||||||||||| |||||||||||||||||||||||
Db   483 GAATTTGTGAAATGTAAAACATCATGGTTTCCATTGAGATGGCATTTT 542

Qy   483 GAATTTGTGAAATGTAAAACATCATGGTTTCCATTGAGATGGCATTTT 542
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   102 AAACCTGTGAAATGTAAGCATCATGGTTTCCATTGGGGATGGCATTTT 43

Qy   102 AAACCTGTGAAATGTAAGCATCATGGTTTCCATTGGGGATGGCATTTT 43
         |||||||||||||||| ||||||| ||||||||| |||||||||||
Db   543 GGTGTGGTCCGTTGAAGCCTTGGCCCGAGGCCGCGGCGGACGCT 584

Qy   543 GGTGTGGTCCGTTGAAGCCTTGGCCCGAGGCCGCGGCGGACGCT 584
         |||||||| ||||||| ||| |||||||||| ||
Db   42 GAAG-AATCTGTTGAAACCTGGGCCCCTGAGGCGCTGCAGTCT 2

Qy   42 GAAG-AATCTGTTGAAACCTGGGCCCCTGAGGCGCTGCAGTCT 2

RESULT 43
RATS100RP/c
LOCUS   RATS100RP   573 bp   mRNA   linear   ROD 27-APR-1993
DEFINITION   Rat S-100 related protein mRNA, complete cds, clone 42C.
ACCESSION   J03627
VERSION   J03627.1 GI:206827
KEYWORDS   S-100-related protein; calcium-binding protein.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE   1 (bases 1 to 573)
AUTHORS   Masiakowski,P. and Shooter,E.M.
TITLE   Nerve growth factor induces the genes for two proteins related to a
               family of calcium-binding proteins in PC12 cells
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (4), 1277-1281 (1988)
MEDLINE   88125019
PUBMED   3422491
COMMENT   Original source text: Rat adrenal pheochromocytoma nerve growth
               factor-induced cell line PC12, cDNA to mRNA, clone 42C.
               Draft entry and computer-readable sequence for [1] kindly provided
               by P.Masiakowski, 04-JAN-1988.
FEATURES   Location/Qualifiers
     source   1..573
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
     mRNA   <1..573
                     /product="S-100-related protein mRNA"
     CDS   46..333
                     /note="S-100-related protein"
                     /codon_start=1
                     /protein_id="AAA42097.1"
                     /db_xref="GI:206828"
                     /translation="MPSQMEHAMETMMLTFHRFAGEKNYLTKEDLRVLMEREFPGFLE
                     NQKDPLAVDKIMKDLDQCRDGKVGFQSFLSLVAGLIIACNDYFVVHMKQKK"
ORIGIN   9 bp upstream of PstI site.

Query Match   27.5%;   Score 329.2; DB 10; Length 573;
Best Local Similarity   78.2%;   Pred. No. 1.1e-59;
Matches 455; Conservative   0; Mismatches 103; Indels 24; Gaps   4;

Qy   7 AAAAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAATCAAAAGCTT 66
         ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   563 AAAAAAGAACTTTCTTTATTGAGGGCAACCGATGCAAACAATATAAAACCGAAAGCTC 504

Qy   67 ATCTGGTAT----TTAACTTTTCTTTTCTTTTCTTTTCTTCAAATGAGATTTTATTTT 122
         ||||||| |||||| ||| |||| || ||| |||||||| ||||||||
Db   503 CTCTGCTCAAGTGCTAAGTGCTCCTGATCTGCATGATGAAATCCTTCTGCCTTGTGGGGC 444

Qy   123 TACATTTGCTAAGTGCTCCTGATCATCGTCGCTCATGATGAAATCCTTCATGGGGGACTGT... 182

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Qy      7 AAAAAAGAACTTTATTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTT 66
          |||||| ||||||||||||||||||||||||| ||||| |||||||||  || |||||
Db    563 AAAAAAAGAACTTTCTTTATTGAGGGCAACCGATGCAAACAATATAAAACTCGAAAGCTC 504

Qy     67 ATCTGGTAT----TTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATTT 122
          ||||       ||||| |||  || ||||||||||||||||||||||||||||| |||||
Db    503 CTCTGTCATTGGATTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATTTG 444

Qy    123 TACATTTGCTAAGTGTCCTGATCTGCTCA-----------CAGGAAGCAGTGGGGC 182
          |||||||||||| |||||||||| ||||||            |||||||||||||||
Db    443 CACATTTGCTAAGTGTCCTGATCTGCTCA-----------CAGGAAGCAGTGGGGC 399

Qy    183 AGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCATTTC 242
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    398 AGATTCCTCAGTTGACCCCATGGGAGAGGACGCATCCAAGGTGTGGGGGAGCGTGGGGC 340

Qy    243 TGCCTACTTCTTTCCTTCTGCTTCATGTGTACTGTACAAAATAGTCATTGCAATGGT 302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 GAGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCACTTTGCCATCTCTACACTGTC 221

Qy    303 GGGAGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCACTTTGCCATCTCTACACTGTGT 362
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 GAGCCCGCCACTAGTGATAGAAAGCTCGGAAGCCCCACTTTTCCATCTCGGCACTGTC 220

Qy    363 CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 161

Qy    423 GAGGCCCGCAATTAGGGAAAGAAGCTCTGAAGCCACTCGGAGC 482
          ||||||||||||||||||||||||||||||||||||||||||
Db    423 GAACTCCTTTCCATGAGTACTCTCAGTCCTCCTTGTTGGTAGCCTTTATCCCCAGC 482

Qy    363 GAGGCCCGCAATTAGGGAAAGAAGCTCTGAAGCCCCACTTTTCCATCTCGGCACTGGTC 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 161

Qy    282 GAGCCCGCCACTAGTGATAGAAAGCTCGGAAGCCCCACTTTTCCATCTCGGCACTGTC 223
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 GAACTCCCTTTCCCATGAGCACTCTCAGTCCTCCTTGTCAAGTAGTTTTTTCCCCTGC 101

Qy    363 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 161

Qy    222 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 161

Qy    423 GAACTCCTTTCCATGAGTACTCTCAGTCCTCCTTGTTGGTAGCCTTTATCCCCAGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 GAACTCCTTTCCATGAGTAAGTTCCATTGAGATGGCATTTT 542

Qy    162 GAACTCCCTTTCCCATGAGCACTCTCAGTCCTCCTTGTCAAGTAGTTTTTTCCCCTGC 103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 GAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATTTT 542

Qy    483 GAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATTTT 542
          ||||||||||||||||||||||||||||||||||||||||||||
Db    100 AAACCTGAAATGTAAGCATCATGGTTTCCATTTGGGATGGCATTTT 41

Qy    102 AAACCTGAAATGTAAGCATCATGGTTTCCATTTGGGATGGCATTTT 43
          |||||||||||||||||||||||||||||||||||||||||||||

Qy    543 GGTGTGGTCCGTTGAAGCCTTGGCCGCCTTGGCCGGAGGCGCCGGCGGCGCT 584
          |||||| |||| |||||||||| ||| || |||||||||||||||||||
Db    543 GGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCGCCGGCGGCCGGA 580

Qy     42 GAAG-AATCTGTTGAAACCTGGGCCTGAGGCGCTGCAGTCT 2
          |||| |||||||||||||||||||||||||| |||||||
Db     40 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCA 4
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RESULT 44
AR489208/c
LOCUS　　　　AR489208　　　　570 bp　　DNA　　linear　　PAT 15-MAY-2004
DEFINITION　Sequence 23 from patent US 6709855.
ACCESSION　 AR489208
VERSION　　 AR489208.1　GI:47256153
KEYWORDS　　.
SOURCE　　　Unknown.
ORGANISM　　Unknown.
　　　　　　Unclassified.
REFERENCE　 1 (bases 1 to 570)
AUTHORS　　 Stanton,L.W., White,R.T., Damm,D.L., Lewicki,J.A., Joly,A. and
　　　　　　Schreiner,G.F.
TITLE　　　 Methods for detection and use of differentially expressed genes in
　　　　　　disease states
JOURNAL　　 Patent: US 6709855-A 23 23-MAR-2004;
FEATURES　　　　　　　Location/Qualifiers
　　source　　　　　　1..570
　　　　　　　　　　　/organism="unknown"
　　　　　　　　　　　/mol_type="genomic DNA"
ORIGIN

Query Match　　　　 27.4%;　Score 328.4;　DB 6;　Length 570;
Best Local Similarity　78.4%;　Pred. No. 1.6e-59;
Matches　453;　Conservative　0;　Mismatches 101;　Indels 24;　Gaps　4;

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Qy      7 AAAAAAGAACTTTATTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTT 66
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Db    561 AAAAAAAGAACTTTCTTTATTGAGGGCAACCGATGCAAACAATATAAAACTCGAAAGCTC 502

Qy     67 ATCTGGTAT----TTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATTT 122
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RESULT 45
AX260435/c
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DEFINITION　Sequence 86 from Patent WO0173027.
ACCESSION　 AX260435
VERSION　　 AX260435.1　GI:16509402
KEYWORDS　　.
SOURCE　　　Homo sapiens (human)
ORGANISM　　Homo sapiens
　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　 1
AUTHORS　　 Meagher,M.J., Xu,J. and King,G.E.
TITLE　　　 Compositions and methods for therapy and diagnosis of colon cancer
JOURNAL　　 Patent: WO 0173027-A 86 04-OCT-2001;
　　　　　　CORIXA CORPORATION (US)
FEATURES　　　　　　　Location/Qualifiers
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　　　　　　　　　　　/mol_type="unassigned DNA"
　　　　　　　　　　　/db_xref="taxon:9606"
ORIGIN

Query Match　　　　 26.4%;　Score 317;　DB 6;　Length 318;
Best Local Similarity　100.0%;　Pred. No. 4e-57;
Matches　317;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

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Db    317 GGGGATGCAAACAATACAAAAATCAAAAATCAAAAGCTTATCTGTATTTTCTTTTCTTTCTCTGC 258

Qy     95 TTGTCAAATGAGAGTTAGATTTTATTTTTATTTGCTAAGTGTCCTGATCTGCTCATGA 154
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257 TTGTCAAATGAGAGTTAGATTTTATTTTTACATTTGCTAAGTGTCCTGATCTGCTCATGA 198

Qy    155 AATCCTTCTATGGGAAGCTGTGGGAGATTCCTTAAGCGACCCTTTGGGACAACTCT 214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   197 AATCCTTCTATGGGGGAAGCTGTGGGCAGATTCCTTAAGCGACCCTTTGGGACAACTCT 138

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Qy   275 CTACAAAATAGTCATTGCATGCAATGGTGAGGCCCCGCAATTAGGGAAAAAGAAGCTCTGGA 334
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Qy   335 AGCCCACTTTGCCATCT 351
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Search completed: August 18, 2005, 05:26:07
Job time : 5219 secs

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               GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    August 17, 2005, 22:29:32 ; Search time 668 Seconds
                              (without alignments)
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Title:          US-10-735-577-16
Perfect score:  1199
Sequence:       1 ggaactaaaaagaacttta.........cgggcttccgcgccccaccgg 1199
Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched:       4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:     8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        10: geneseqn2003cs:*
        11: geneseqn2003ds:*
        12: geneseqn2004as:*
        13: geneseqn2004bs:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1199	100.0	1199	12	ADP67435	Adp67435 Human p11
2	1199	100.0	1199	12	ADP67436	Adp67436 Human p11
3	1199	100.0	1199	12	ADQ84359	Adq84359 Human tum
4	1199	100.0	1199	13	ACN37451	Acn37451 Tumour-as
5	703.4	58.7	1124	8	ABX63001	Abx63001 Human cDN
6	634	52.9	1893	3	AAC78192	Aac78192 Human can
7	634	52.9	1893	4	AAF75079	Aaf75079 Human col
8	601	50.1	649	3	AAA46679	Aaa46679 cDNA of a
9	601	50.1	649	6	ABN95852	Abn95852 Gene #235
10	601	50.1	649	10	ADD18599	Add18599 Human dis
11	601	50.1	649	10	ADF81436	Adf81436 Leukaemia
12	601	50.1	649	10	ABX13104	Abx13104 Human cDN
13	601	50.1	649	13	ADR24986	Adr24986 Breast ca
14	601	50.1	649	13	ADP54125	Adp54125 Human PRO
15	601	50.1	649	13	ADS17592	Ads17592 Nucleotid
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18	537	44.8	571	6	ABK45339	Abk45339 cDNA enco
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21	485.2	40.5	2016	8	ACC51060	Accs1060 Human S-1
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24	422	35.2	466	9	ACH25344	Ach25344 Human adu
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ALIGNMENTS

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ID   ADP67435 standard; cDNA; 1199 BP.
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AC   ADP67435;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human p11 antisense polynucleotide SEQ ID NO:16.
XX
KW   p11; p11 activity modulator; plasminogen activation; cytostatic;
KW   antisense therapy; cancer; tumour; tumour growth inhibition; human;
KW   antisense; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200054517-A2.
XX
PD   01-JUL-2004.
XX
PF   12-DEC-2003; 2003WO-US040029.
XX
PR   13-DEC-2002; 2002US-0433140P.
XX
PA   (MEDI-) MEDIOMICS LLC.
PA   (WAIS/) WAISMAN D.
XX
PI   Waisman D;
XX
DR   WPI; 2004-487995/46.
XX
PT   Composition useful for inhibiting growth of tumor in patient, modulates
PT   activity of p11 protein and effects a change in level of plasminogen
PT   activation by a cell.
XX
PS   Claim 5; SEQ ID NO 16; 140pp; English.
XX
CC   The present invention describes a composition (I) which modulates the
CC   activity of a p11 protein and effects a change in the level of
CC   plasminogen activation by a cell. Also described: (1) making (M1) a
CC   clonal cell line, which involves isolating a cell, then characterising
CC   the activity of a protein produced by the cell or clonal progeny of the
CC   cell, where the protein is involved in plasminogen activation; and (2) a
```

CC   clonal cell line (II) useful in the identification of composition that
CC   modulate p11 activity, where the clonal cell line is obtained by (M1).
CC   (I) has cytostatic activity, and can be used in antisense therapy. (I) is
CC   useful for modulating the activity of p11 which involves administering
CC   (I) to a cell. The cell can be a human cancer cell, chosen from a HT1080
CC   fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal
CC   adenocarcinoma cell. (I) is also useful for reducing the development of
CC   cancer in a patient e.g., mouse which involves administering (I) to a
CC   cancer cell in the patient. (I) is useful for inhibiting the growth of
CC   tumours or inhibiting tumour cell invasion in a patient, which involves
CC   administering (I) to a cancer cell in the patient. (II) is useful for
CC   identifying a composition that modulates p11 activity which involves
CC   administering the composition to (II) obtained by (M1), determining the
CC   change in p11 activity of a cell of the clonal cell line relative to a
CC   cell of a clonal cell line that had not received the composition, and
CC   identifying the composition that produces a change in p11 activity. The
CC   change in p11 activity is a change in the level of plasminogen activation
CC   activity. The present sequence represents a p11 antisense polynucleotide,
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 1199 BP; 235 A; 338 C; 337 G; 289 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1199;   DB 12;   Length 1199;
Best Local Similarity   100.0%;   Pred. No. 3.3e-293;
Matches 1199;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Db     1 GGAACTAAAAAGAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  60

Qy    61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db    61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120

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Db   301 GTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGGAAGCCCATCTCTACACTGG 360

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Db   661 GGGTGGTAGAGGGAGGAGGCGGCGCGGGAGCGGGAGCGGCGGGAGCCTGGCGCGGGCGGGCTCGGCGCAGGGGCG 720

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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GAACCCGGCCGTCCTGCGGGTGGGGCACGCGTGGGGCACGCGTGGGCCAGAGAGTGGCCTCGC 1020

Qy  1021 GGCCACCTACGGGTCTAGGAATTACTTGCTCGATGAACCCTGCAGGGAGTGGCACGTGGAG 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGCCACCTACGGGTCTAGGAATTACTTGCTCGATGAACCCTGCAGGGAGTGGCACGTGGAG 1080

Qy  1081 TCCTATCGACCTCAGAGGCACTATCAGATTAGCCCTAGGAGTCCGTCTGGGGGTCTCGG 1140
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Db  1141 CGGCCTGCGCGCCAGTGAGGGGCGGCGCACCTCCCAGAAGCCGGGCTTCCCGCCCCACCGG 1199
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RESULT 2
ADP67436/c
ID   ADP67436 standard; cDNA; 1199 BP.
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AC   ADP67436;
XX
DT   23-SEP-2004 (first entry)
XX
DE   Human p11 sense polynucleotide SEQ ID NO:17.
XX
KW   p11; p11 activity modulator; plasminogen activation; cytostatic;
KW   antisense therapy; cancer; tumour; tumour growth inhibition; human; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200454517-A2.
XX
PD   01-JUL-2004.
XX
PF   12-DEC-2003; 2003WO-US040029.
XX
PR   13-DEC-2002; 2002US-0433140P.
XX
PA   (MEDI-) MEDIOMICS LLC.
PA   (WAIS/) WAISMAN D.
XX
PI   Waisman D;
XX
DR   WPI; 2004-487995/46.
XX
PT   Composition useful for inhibiting growth of tumor in patient, modulates
PT   activity of p11 protein and effects change in level of plasminogen
PT   activation by a cell.
XX
PS   Claim 16; SEQ ID NO 17; 140pp; English.
XX
CC   The present invention describes a composition (I) which modulates the
CC   activity of a p11 protein and effects a change in the level of

CC   plasminogen activation by a cell. Also described: (1) making (M1) a
CC   clonal cell line, which involves isolating a cell, then characterising
CC   the activity of a protein produced by the cell or clonal progeny of the
CC   cell, where the protein is involved in plasminogen activation; and (2) a
CC   clonal cell line (II) useful in the identification of composition that
CC   modulate pli activity, where the clonal cell line is obtained by (M1).
CC   (I) has cytostatic activity, and can be used in antisense therapy. (I) is
CC   useful for modulating the activity of pli which involves administering
CC   (I) to a cell. The cell can be a human cancer cell, chosen from a HT1080
CC   fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal
CC   adenocarcinoma cell. (I) is also useful for reducing the development of
CC   cancer in a patient e.g., mouse which involves administering (I) to a
CC   cancer cell in the patient. (I) is useful for inhibiting the growth of
CC   tumours or inhibiting tumour cell invasion in a patient, which involves
CC   administering (I) to a cancer cell in the patient. (II) is useful for
CC   identifying a composition that modulates pli activity which involves
CC   administering the composition to (II) obtained by (M1), determining the
CC   change in pli activity of a cell of the clonal cell line relative to a
CC   cell of a clonal cell line that had not received the composition, and
CC   identifying the composition that produces a change in pli activity. The
CC   change in pli activity is a change in the level of plasminogen activation
CC   activity. The present sequence represents a pli sense polynucleotide,
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 1199 BP; 289 A; 337 C; 338 G; 235 T; 0 U; 0 Other;

Query Match   100.0%; Score 1199; DB 12; Length 1199;
Best Local Similarity 100.0%; Pred. No. 3.3e-293;
Matches 1199;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db   1199 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATCCAAACAATACAAAAATACAAATCAA 1140

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
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Db   1079 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 1020

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Qy   241 TCTGCCTACTTCTTTCCCTTGCTTCATGTGTACTACAAAAATAGTCATTGCCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   959 TCTGCCTACTTCTTTCCCTTGCTTCATGTGTACTACAAAAATAGTCATTGCCATGCAATG 900

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   839 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 780

Qy   421 GGGAACTCCTTTTCATGAGTACTCTCAGGTGCCCTTAAGTAGCCTTTATCCCA 480
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Db   779 GGGAACTCCTTTTCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCA 720

Qy   481 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   719 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 660

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCCGACGGCTGGGCGAG 600
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Db   659 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCCGACGGCTGGGCGAG 600

Qy   601 CTTGGACGCGCGGGCGGGAGAGGCGAGCGGCGGCGGGCTGTGCCGCCTTCCTTAGTACGTGCGGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 CTTGGACGCGCGGGCGGGAGAGGCGAGCGGCGGCGGGCTGTGCCGCCTTCCTTAGTACGTGCGGC 540

Qy   661 GGGTGGGTAGAGGGAGGGAGGCGGCGGGGAGGAGGCTGGCGGCGGCTGGCGGCGGCTGGCGGCGGCTCGGCGGCAGGGCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539 GGGTGGGTAGAGGGAGGGAGGCGGCGGGGAGGAGGCTGGCGGCGGCTGGCGGCGGCTGGCGGCGGCTCGGCGGCAGGGCG 480

Qy   721 CTCCCCCAGCCGTCTCCTCCTCCTCCGCTGCCCGACTCCCCCGACCCCCGGGCGCGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 CTCCCCCAGCCGTCTCCTCCTCCTCCGCTGCCCCGACTCCCCCGACCCCCGGGCGCGG 420

Qy   781 CGGCCACGCGCCTCGCCTCGCCTCGCCTCCGAGACCCGCCTCGCCGCTCCGCGCCCGCCGCCCCGAGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419 CGGCCACGCGCCTCGCCTCGCCTCCGACCCCGCCTCGCCGCTCCGCAGAGGCCTCGCCGCTCCGCCAGAC 360

Qy   841 AGAGCGTTCTGTAAACTTCTCAGTAGAAACGGTCCTGCTTCTCGAATATTTCAGGGC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 AGAGCGTTCTGTAAACTTCTCAGTAGAAACGGTCCTGCTTCTCGAATATTTCAGGGC 300

Qy   901 ATCCCCACCCTGAGCCTGCCCTTCCTCGGGTTGGTTTAGAAAAGTGTACAAAATCAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 ATCCCCACCCTGAGCCTGCCCTTCCTCGGGTTGGTTTAGAAAAGTGTACAAAATCAA 240

Qy   961 GAACCCGGCCGTCCTGCGGGTGGGGCACGCTGCGCAGAACCAGAGGTAACCAGGGTAACCGGCTCTGC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 GAACCCGGCCGTCCTGCGGGTGGGGCACGCTGCGCAGAACCAGAGGTAACCAGGGTAACCGGCTCTGC 180

Qy   1021 GGCCACTTACGGGTCTAGGAATTACTTGCTGATGACCCTGCAGGGAGTGGCACGTGGAG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 GGCCACTTACGGGTCTAGGAATTACTTGCTGATGACCCTGCAGGGAGTGGCACGTGGAG 120

Qy   1081 TCCTATGACCTCAGAGCACTATCAGATTAGCCTCCTAGGAGGTCCGTCTGGGGTCTCGG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 TCCTATGACCTCAGAGCACTATCAGATTAGCCTCCTAGGAGGTCCGTCTGGGGTCTCGG 60

Qy   1141 CGGCCTGCGCCAGTGAGGGGCGGCCACCTCCCCAGAGCCCGGCTTCCCGCCCCCACCCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 CGGCCTGCGCCAGTGAGGGGCGGCCACCTCCCCAGAGCCCGGCTTCCCGCCCCCACCCG 1

RESULT 3
ADQ84359/c
ID   ADQ84359 standard; cDNA; 1199 BP.
XX
AC   ADQ84359;
XX
DT   07-OCT-2004 (first entry)
XX
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #1173.
XX
KW   human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW   cancer; cell proliferative disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004060270-A2.
XX
PD   22-JUL-2004.
XX
PF   15-OCT-2003; 2003WO-US029126.
XX
PR   18-OCT-2002; 2002US-0418988P.
XX
PA   (GETH) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
XX
PI   Wu TD, Zhou Y;
XX
DR   WPI; 2004-534300/51.
XX
PT   New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT   preventing or treating cell proliferative disorders such as cancer.
XX
PS   Claim 1; SEQ ID NO 1173; 5504pp; English.

XX
CC   The present invention describes an isolated tumour-associated antigenic
CC   target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC   sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC   (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC   sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC   (c). Also described: (1) an expression vector comprising the above
CC   nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC   a process for producing a polypeptide; (4) an isolated polypeptide
CC   comprising: (a) an amino acid sequence encoded by any of the above
CC   nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC   length coding region of the above nucleotide sequences; or (c) a sequence
CC   having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC   comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC   an isolated antibody that binds to the above polypeptide; (7) a process
CC   for producing the antibody; (8) an isolated oligopeptide that binds to
CC   the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC   binding organic molecule that binds to the above polypeptide; (10) a
CC   composition of matter comprising the above (chimeric) polypeptide,
CC   antibody, oligopeptide or TAT binding organic molecule, in combination
CC   with a carrier; (11) an article of manufacture comprising a container and
CC   the composition of matter contained within the container; (12) methods of
CC   inhibiting the growth of a cell that expresses the above protein, where
CC   the growth of the cell is at least in part dependent upon a growth
CC   potentiating effect of the above protein; (13) a method of
CC   therapeutically treating a mammal having a cancerous tumour comprising
CC   cells that express the above protein; (14) a method of determining the
CC   presence of a protein in a sample suspected of containing the protein
CC   described above; (15) methods of diagnosing the presence of a tumour in a
CC   mammal; (16) a method for treating or preventing a cell proliferative
CC   disorder associated with increased expression or activity of the above
CC   protein; and (17) a method of binding an antibody, oligopeptide or
CC   organic molecule to a cell that expresses the protein described above.
CC   The TAT sequences have cytostatic activities, and can be used in gene
CC   therapy. The composition and methods are useful for diagnosing,
CC   preventing or treating cancer. The composition is also used for preparing
CC   a medicament for the therapeutic treatment or diagnostic detection of a
CC   cell proliferative disorder or cancer. The present sequence represents a
CC   human TAT cDNA sequence from the present invention.
XX
SQ   Sequence 1199 BP; 289 A; 337 C; 338 G; 235 T; 0 U; 0 Other;

Query Match   100.0%; Score 1199; DB 12; Length 1199;
Best Local Similarity   100.0%;
Matches 1199; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 1140

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCTGCTTGTGTCTTGTCAAATGAGAGTTAGAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 AAGCTTATCTGGTATTTAACTTTCTTCTTCTCTGCTTGTGTCTTGTCAAATGAGAGTTAGAGATTTTATT 1080

Qy   121 TTTACATTGCTAAGTGTCCTGATCGTCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 TTTACATTGCTAAGTGTCCTGATCGTCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 1020

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 960

Qy   241 TCTGCTACTTCTTCTTCCCTTCTGCGTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   959 TCTGCTACTTCTTCTTCCCTTCTGCGTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 900

Qy   301 GTGAGGCCCGCAATTAGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   899 GTGAGGCCCGCAATTAGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 840

Qy   361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   839 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 780

Qy   421 GGGAACTCCTTTCATGAGTACTTCTCAGTTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   779 GGGAACTCCTTTCATGAGTACTTCTCAGTTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 720

Qy   481 GCGAATTGTGAAATGTAAACATCATGGTTCCATGCGGTGTTCCATTGAGATGGCATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   719 GCGAATTGTGAAATGTAAACATCATGGTTCCATGCGGTGTTCCATTGAGATGGCATT 660

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGGGACGCTGGGCGAGCTGGGCGAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   659 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGGGACGCTGGGCGAGCTGGGCGAG 600

Qy   601 CTTGGACGCGGGGGCGGAGAGGCGGAGGAGCGCGGGCGGGTGTGCGCCTTCCTTAGTACGTGCGGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 CTTGGACGCGGGGGCGGAGAGGCGGAGGAGCGCGGGCGGGTGTGCGCCTTCCTTAGTACGTGCGGC 540

Qy   661 GGGTGGGTAGAGGAGGAGCGCGGGCGGGCGGGCGGGCGGGGGGCGGCTCGCGGCGCTCGCGGCAGGGCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539 GGGTGGGTAGAGGAGGAGCGCGGGCGGGCGGGCGGGCGGGGGGCGGCTCGCGGCGCTCGCGGCAGGGCG 480

Qy   721 CTCCCCAGCCCGTCTCCTCCCGCTCCGGACCCGCCTCGCAGAGGCCCGCGCCCCCGGGCCCCAGAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 CTCCCCAGCCCGTCTCCTCCCGCTCCGGACCCGCCTCGCAGAGGCCCGCGCCCCCGGGCCCCAGAC 420

Qy   781 CGGCCCACGCCCTGCCCTGCTTCCGGACCCGCCTCGCAGAGGCCCTGCGGCCTGCGAATATTTCAGGGC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419 CGGCCCACGCCCTGCCCTGCTTCCGGACCCGCCTCGCAGAGGCCCTGCGGCCTGCGAATATTTCAGGGC 360

Qy   841 AGAGCGTTCTTGTAAACTTCTTCAGTAGAAACGGTTCCTGCTCTCGAATATTTCAGGGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 AGAGCGTTCTTGTAAACTTCTTCAGTAGAAACGGTTCCTGCTCTCGAATATTTCAGGGC 300

Qy   901 ATCCCCACCCTGAGCCTGCCCTTCCTCCTCGGGTTTGTTTTAGAAAGTGTACAAATCAAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 ATCCCCACCCTGAGCCTGCCCTTCCTCCTCGGGTTTGTTTTAGAAAGTGTACAAATCAAA 240

Qy   961 GAACCCGGCCGTCCTGCGGGTGGGCACGTGGGCCGCAGAACCAGAGGTAACCGGCTCTGC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 GAACCCGGCCGTCCTGCGGGTGGGCACGTGGGCCGCAGAACCAGAGGTAACCGGCTCTGC 180

Qy   1021 GGCCACCTACGGGTCTAGGAATTACTTGCTTGGATGACCCTGCACGGTGCACGTGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 GGCCACCTACGGGTCTAGGAATTACTTGCTTGGATGACCCTGCACGGTGCACGTGGAG 120

Qy   1081 TCCTATCGACCTCAGAGGCACTATCAGATTAGCCTTAGGGGGTCTCGG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   119 TCCTATCGACCTCAGAGGCACTATCAGATTAGCCTTAGGGGGTCTCGG 60

Qy   1141 CGGCCTGCGCCAGTGAGGGGGCGGCACCTCCCCAGAAGCCCGGGCTTCCCGCCCCACCGG 1199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 CGGCCTGCGCCAGTGAGGGGGCGGCACCTCCCCAGAAGCCCGGGCTTCCCGCCCCACCGG 1

RESULT 4
ACN37451/c
ID   ACN37451 standard; cDNA; 1199 BP.
XX
AC   ACN37451;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Tumour-associated antigenic target (TAT) cDNA DNA323900, SEQ ID NO:342.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
KW   gene therapy; cytostatic; gene; ss.
XX
OS   Homo sapiens.

```
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD, Zhang Z, Zhou Y;
XX
DR   WPI; 2004-347921/32.
DR   P-PSDB; ABM80135.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 1; SEQ ID NO 342; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT nucleic acid of the invention
XX
SQ   Sequence 1199 BP; 289 A; 337 C; 338 G; 235 T; 0 U; 0 Other;

Query Match     100.0%;     Score 1199;  DB 13;  Length 1199;
Best Local Similarity   100.0%;  Pred. No. 3.3e-293;
Matches 1199;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGGATCAAACAATACAAAAATCAA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGGATCAAACAATACAAAAATCAA 1140

Qy     61 AAGCTTATCTCGGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 AAGCTTATCTCGGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTTTATT 1080

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 1020

Qy    181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 960

Qy    241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 900

Qy    301 GTGAGGCCCGCAATTAGGGAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 GTGAGGCCCGCAATTAGGGAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 840

Qy    361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 780

Qy    421 GGGAACTCCTTTTCCATGAGTACTCCAGTGCTCTCAGTTAAGTAGCCTTTATCCCCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 GGGAACTCCTTTTCCATGAGTACTCCAGTGCTCTCAGTTAAGTAGCCTTTATCCCCA 720

Qy    481 GCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 540
          |||||||||||||||||||||||||||||||||||||||||||||
Db    719 GCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 660

Qy    541 TTGGTGTGGTCCGTGAAGCCTTGGCCGAGGCGCGGCGACCGTGGGCGGAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 TTGGTGTGGTCCGTGAAGCCTTGGCCGAGGCGCGGCGACCGTGGGCGGAG 600

Qy    601 CTGGACGCGGGGGCGGAGGGGAGCGGAGGGCCGGCCTTCCTTAGTACGTGCGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 CTGGACGCGGGGGCGGAGGGGAGCGGAGGGCCGGCCTTCCTTAGTACGTGCGC 540

Qy    661 GGGTGGGTAGAGGGAGGGAGGCCGGCGGGCGGAGGAGCGGCCTCGGCGGGGCTCGGCAGGCG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 GGGTGGGTAGAGGGAGGGAGGCCGGCGGGCGGAGGAGCGGCCTCGGCGGGGCTCGGCAGGCG 480

Qy    721 CTCCCCAGCCGTGTCTCCTCCGCCCTCTTCCTGCCCCGACTCCCCGGCGGCG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 CTCCCCAGCCCGTGTCTCCTCCGCCCTCTTCCTGCCCCGACTCCCCGGCGGCG 420

Qy    781 CGGCCCACGCCCTCCGCTCCGGACCCGCCTCGCCAGAGGCCTCGCCCCCAGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 CGGCCCACGCCCTCCGCTCCGGACCCGCCTCGCCAGAGGCCTCGCCCCCAGAC 360

Qy    841 AGAGGCGTTCTTGTAAACTTCTTCAGTAGAAACGGTCCTGCTCTCGAATATTCAGGGC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 AGAGGCGTTCTTGTAAACTTCTTCAGTAGAAACGGTCCTGCTCTCGAATATTCAGGGC 300

Qy    901 ATCCCCACCCTGAGCCTGCCCTTCCTCCGGTTGGTTTTAGAAGTGTACAAATCAAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 ATCCCCACCCTGAGCCTGCCCTTCCTCCGGTTGGTTTTAGAAGTGTACAAATCAAA 240

Qy    961 GAACCCCGCCGTCCTGCGGGTGGGGCACGCTGCGCAGAACCAGAGGTAACCGGCTCTGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 GAACCCCGCCGTCCTGCGGGTGGGGCACGCTGCGCAGAACCAGAGGTAACCGGCTCTGC 180

Qy   1021 GGCCACCTACGGTCTAGGAATTACTTGCTGATGACCCTGCAGGGAGTGGCACGTGGAG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    179 GGCCACCTACGGTCTAGGAATTACTTGCTGATGACCCTGCAGGGAGTGGCACGTGGAG 120

Qy   1081 TCCTATCGACCTCAGAGCACTATCAGATTAGCCTCAGGAGTCCGTCTGGGGGTCTCGG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119 TCCTATCGACCTCAGAGCACTATCAGATTAGCCTCAGGAGTCCGTCTGGGGGTCTCGG 60

Qy   1141 CGGCCTGCGCCAGTGAGGGGGGCGCACCTCCCCAGAGCGCCGGGCTTCCCGCCCCACCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59 CGGCCCTGCGCCAGTGAGGGGGGCGCACCTCCCCAGAGCGCCGGGCTTCCCGCCCCACCG 1

RESULT 5
ABX63001/c
ID   ABX63001 standard; cDNA; 1124 BP.
XX
AC   ABX63001;
XX
DT   25-FEB-2003  (first entry)
XX
DE   Human cDNA #1 differentially expressed in activated vascular tissue.
XX
KW   Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
KW   hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
KW   gene therapy; vascular disease; cancer; coronary; artery disease;
KW   hypertension; diabetes; pre-eclampsia; restenosis;
KW   ischaemia-reperfusion injury; stroke.
```

```
XX
OS   Homo sapiens.
XX
PN   US2002137081-A1.
XX
PD   26-SEP-2002.
XX
PF   08-JAN-2002; 2002US-00044090.
PR   28-JUL-2000; 2000US-0222469P.
PR   08-JAN-2001; 2001US-0260483P.
XX
PA   (BAND/) BANDMAN O.
XX
PI   Bandman O;
XX
DR   WPI; 2003-110597/10.
XX
PT   Combination for diagnosing, staging, treating, or monitoring the
PT   progression of treatment of a vascular disease, e.g. atherosclerosis,
PT   comprises several cDNAs that are differentially expressed in activated
     vascular tissue.
XX
PS   Claim 1; Page 1; 18pp; English.
XX
CC   This invention relates to a combination comprising several cDNAs that are
CC   differentially expressed in activated vascular tissue. The invention also
CC   discloses a high throughput method for detecting differentially expressed
CC   cDNAs in a sample. The cDNAs of the invention may have
CC   antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;
CC   gynaecological; vasotropic and cerebroprotective activities and may be
CC   used in gene therapy. The cDNAs of the invention may be used in a high-
CC   throughput methods for detecting differential expression of one or more
CC   cDNAs in a sample, or screening several molecules or compounds to
CC   identify a molecule or compound that specifically binds a cDNA of the
CC   invention. A protein encoded by the cDNA may be used to screen several
CC   molecules or compounds to identify a ligand that specifically binds to
CC   the protein, or to produce or purify an antibody to the protein that can
CC   be used to detect a protein in a sample or purify a natural or
CC   recombinant protein from a sample. The nucleotides may be useful for
CC   diagnosing, staging, treating, or monitoring the progression of treatment
CC   of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
CC   disease, hypertension, diabetes, pre-eclampsia, ischaemia- reperfusion
CC   injury, restenosis, or stroke. The cDNAs can also be used for large-scale
CC   genetic or gene expression analysis of several new nucleic acid
CC   molecules. Antibodies to the proteins encoded by the cDNAs are useful for
CC   diagnosing pre-pathologic disorders, and chronic or acute diseases
CC   associated with abnormalities in the expression, amount or distribution
CC   of the protein. The present sequence represents a cDNA of the invention
CC   that is differentially expressed in activated vascular tissue. Note: The
CC   sequence data for this patent did not form part of the specification, but
CC   was obtained in electronic format directly from USPTO at
CC   http:seqdata.uspto.gov/sequence.html?DocID=20020137081
XX
SQ   Sequence 1124 BP; 320 A; 286 C; 261 G; 254 T; 0 U; 3 Other;

Query Match            58.7%;  Score 703.4;  DB 8;  Length 1124;
  Best Local Similarity   98.6%;
  Matches  723;  Conservative    0;  Mismatches    1;  Indels    9;  Gaps     1;

Qy          1 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 674

Qy         61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 614

Qy        121 TTTACATTTGCTAAGTGTCCTAAGTCGATCTGCTCATCGTCATCTTCTATGGGGAAGCTGTGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 TTTACATTTGCTAAGTGTCCTAAGTCGATCTGCTCATCGTCATCTTCTATGGGGAAGCTGTGGG 554

Qy        181 GCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT 494

Qy        241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 434

Qy        301 GTGAGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GTGAGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 374

Qy        361 TCCAGGTCCTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TCCAGGTCCTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 314

Qy        421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCTTTATCCCCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCTTTATCCCCA 254

Qy        481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GCGAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 194

Qy        541 TTGGTGTGGTCCGTTGGAAGCCTTGGCCGAGGCGCGGGAC-------GCTGGGGCGAG 591
              ||||||||||||||||| ||||||||||||||||||||||       ||||||||||||
Db        193 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGGACGCGGGGAGCCTGGGGCGAG 134

Qy        592 CTGGGGCCAGCTGGACGCGGGGGGAGAGGCGGAGCCGCGGCGCGTGCGCCTTCCTAGT 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        133 CTGGGGCCAGCTGGACGCGGGGGGAGAGGCGGAGCCGCGGCGCGTGCGCCTTCCTTAGT 74

Qy        652 ACGTGCGGCGGGTGGTGGTAGAGGGAGGGGAGCCGGAGCGGAGGAGCCTGGCGGGCGCTC 711
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         73 ACGTGCGGCGGGTGGTGGTAGAGGGAGGGGTGCGGAGGAGCCTGGCGGGCGCTC 14

Qy        712 GGCAGGGCGCTCC 724
              |||||||||||||
Db         13 GGCAGGGCGCTCC 1

RESULT 6
AAC78192/c
ID   AAC78192 standard; cDNA; 1893 BP.
XX
AC   AAC78192;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human cancer associated gene sequence SEQ ID NO:586.
XX
KW   Human; cancer associated gene; cancer antigen; detection; cancer;
KW   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW   antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW   antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW   dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW   vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW   immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW   allergic reaction; graft versus host disease; organ rejection;
KW   haemostatic; thrombolytic; cardiovascular disorder; infection;
KW   neurological disease; drug screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055350-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005882.
XX
PR   12-MAR-1999;  99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
```

PI   Rosen CA, Ruben SM;
XX
DR   WPI; 2000-587533/55.
DR   P-PSDB; AAB43983.
XX
PT   Novel isolated nucleic acids comprising sequences encoding peptides
PT   useful for treating or diagnosing e.g. cancer.
XX
PS   Claim 1; Page 1108-1109; 2352pp; English.
XX
CC   AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC   AAB43338 to AAB4239. The proteins can have activities based on the
CC   tissues and cells the genes are expressed in. Example of activities
CC   include: cytostatic; proliferative; vulnerary; immunomodulator;
CC   antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC   antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC   dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC   nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC   polynucleotides and polypeptides can be used for preventing, treating or
CC   ameliorating medical conditions and diagnosing pathological conditions.
CC   Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC   the present invention may be used to treat immune disorders by activating
CC   or inhibiting the proliferation, differentiation or mobilisation of
CC   immune cells, to treat disorders of haematopoietic cells, autoimmune
CC   disorders, allergic reactions, graft versus host disease and organ
CC   rejection, modulate haemostatic or thrombolytic activity, modulate
CC   inflammation, cancers, cardiovascular disorders, neurological disease and
CC   bacterial or viral infections. The peptides, nucleotides, antibodies,
CC   agonists and antagonists may be also be used in drug screens. AAC78449 to
CC   AAC78457 and AAB4240 represent sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 1893 BP; 543 A; 466 C; 419 G; 458 T; 0 U; 7 Other;

Query Match   52.9%; Score 634; DB 3; Length 1893;
Best Local Similarity   100.0%; Pred. No. 5.1e-150;
Matches 634; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGAACTAAAAAAGAACTTATTAATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1836 GGAACTAAAAAAGAACTTATTAATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 1777

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTTCTTTCTTGTCAAATGAGAGTTAGATTTTATT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1776 AAGCTTATCTGGTATTTAACTTTCTTTTCTTTCTTGTCAAATGAGAGTTAGATTTTATT 1717

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCAGGGAGGAAGCTGTGGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1716 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCAGGGAGGAAGCTGTGGG 1657

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGACGAACTGCTCATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGACGAACTGCTCATT 1597

Qy   241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1596 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 1537

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 1477

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 1417

Qy   421 GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416 GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 1357

Qy   481 GGGAATTTGTGAAAATGTAAACATCATGTTCCATTGGCTGTGTTCCATTGAGATGGCATT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356 GCGAATTTGTGAAAATGTAAACATCATGTTCCATTGGCGCTGTTCCATTGAGATGGCATT 1297

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGGCGCCGAGGGCGCGGCGACGGCTGGGCGGAGCTGGGGAG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296 TTGGTGTGGTCCGTTGAAGCCTTGGCGCCGAGGGCGCGGCGACGGCTGGGCGGAGCTGGGGAG 1237

Qy   601 CTCGACGCGGGGCGGGGCGGAGAGGCGAGAGGCGCGGCGGGC 634
            ||||||||||||||||||||||||||||||||||||||||||
Db   1236 CTCGACGCGGGGCGGGGCGGAGAGGCGAGAGGCGCGGCGGGC 1203

RESULT 7
AAF75079/c
ID   AAF75079 standard; cDNA; 1893 BP.
XX
AC   AAF75079;
XX
DT   10-MAY-2001 (first entry)
XX
DE   Human colon associated protein cDNA sequence #3.
XX
KW   Human; colon; cancer; disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO20012781-A1.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022157.
XX
PR   13-AUG-1999;   99US-0148680P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CB, Rosen CA;
XX
DR   WPI; 2001-147551/15.
XX
PT   Nucleic acids encoding 13 human colon cancer associated polypeptide,
PT   useful for preventing, diagnosing and/or treating e.g. cancers
PT   (especially colon cancer), Parkinson's disease and diabetic retinopathy.
XX
PS   Claim 1; Page 308-309; 326pp; English.
XX
CC   The present invention relates to 13 human colon cancer-associated
CC   proteins. These proteins and the nucleic acid encoding them may be used
CC   in the prevention, diagnosis and treatment of diseases associated with
CC   inappropriate colon cancer-associated protein expression
XX
SQ   Sequence 1893 BP; 543 A; 466 C; 419 G; 458 T; 0 U; 7 Other;

Query Match   52.9%; Score 634; DB 4; Length 1893;
Best Local Similarity   100.0%; Pred. No. 5.1e-150;
Matches 634; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGAACTAAAAAAGAACTTATTAATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1836 GGAACTAAAAAAGAACTTATTAATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 1777

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTTCTTTCTTGTCAAATGAGAGTTAGATTTTATT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1776 AAGCTTATCTGGTATTTAACTTTCTTTTCTTTCTTGTCAAATGAGAGTTAGATTTTATT 1717

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAGCTGTGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1716 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAGCTGTGG 1657

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 GCAGATTCCTTAAGCGACCCTTTGGGACAAACTCTTATCAGGGAGGAGCGAACTGCTCATT 1597

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 GCAGATTCCTTAAGCGACCCTTTGGGACAAACTCTTATCAGGGAGGAGCGAACTGCTCATT 1597

Qy   241 TCTGGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1596 TCTGGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 1537

Qy   301 GTGAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536 GTGAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 1477

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 1417

Qy   421 GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGACGAACTGCTCATT 1357

Qy   241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 GCGAATTTGTGAAAATGTAAACATCATGTTCCATTGGCGCTGTTCCATTGAGATGGCATT 1297

```
Db   1596  TCTGCCTACTCTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 1537
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301  GTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG  360
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536  GTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 1477

Qy    361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  420
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 1417

Qy    421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCA  480
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCA 1357

Qy    481  GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT  540
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356  GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 1297

Qy    541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGACGCGTGGGCGAGCTGGGCGAG  600
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGACGCGTGGGCGAGCTGGGCGAG 1237

Qy    601  CTGGACGCGGGGCGGAGAGGCGAGCGCGGCGGGC  634
                  ||||||||||||||||||||||||||||||||||
Db   1236  CTGGACGCGGGGCGGAGAGGCGAGCGCGGCGGGC 1203
```

RESULT 8
AAA46679/c
ID   AAA46679 standard; cDNA; 649 BP.
XX
AC   AAA46679;
XX
DT   25-SEP-2000 (first entry)
XX
DE   cDNA of a human gene encoding cellular ligand of annexin II.
XX
KW   Differentially expressed human gene; cardiac disease; kidney disease;
KW   inflammatory disease; I-8U; prostacyclin-stimulating factor; isF-2;
KW   tissue specific mRNA; insulin-like growth factor binding protein 6;
KW   OSF-1; gas-1; YMP; BTG2; pre-B cell stimulating factor homologue; SDF1a;
KW   peripheral benzodiazepine receptor; annexin II cellular ligand; p11;
KW   congenital heart failure; dilated congestive cardiomyopathy;
KW   hypertrophic cardiomyopathy; restrictive cardiomyopathy;
KW   mitral valve disease; aortic valve disease; tricuspid valve disease;
KW   angina pectoris; myocardial infarction; cardiac arrhythmia;
KW   pulmonary hypertension; arterial hypertension; renovascular hypertension;
KW   arteriosclerosis; atherosclerosis; cardiac tumour; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   112..405
FT   /*tag= a
XX
PN   WO200035473-A2.
XX
PD   22-JUN-2000.
XX
PF   15-DEC-1999; 99WO-US029941.
XX
PR   18-DEC-1998; 98US-0113008P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Stanton LW, White RT, Damm DL, Lewicki JA, Joly A, Schreiner GF;
XX
DR   WPI; 2000-451904/39.
DR   P-PSDB; AAY93605.
XX
PT   Preventing, diagnosing and treating cardiac, kidney and inflammatory
PT   disorders using cardiac genes that are differentially expressed in
PT   disease states such as cardiac arrhythmia and arteriosclerosis.

XX
PS   Disclosure; Fig 7L; 170pp; English.
XX
CC   AAA46668-79 represent differentially expressed human genes, associated
CC   with disease states and disorders. The specification describes methods
CC   preventing, diagnosing and treating cardiac, kidney and inflammatory
CC   diseases associated with inappropriate expression of differentially
CC   expressed cardiac, kidney and inflammatory genes (e.g. AAA46668-79).
CC   These genes include I-8U; prostacyclin-stimulating factor; isF-2; tissue
CC   specific mRNA, insulin-like growth factor binding protein 6, OSF-1, gas-
CC   1, YMP, BTG2, pre-B cell stimulating factor homologue (SDF1a), peripheral
CC   benzodiazepine receptor, and cellular ligand of annexin II (p11)
CC   respectively. These diseases include congenital heart failure, dilated
CC   congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive
CC   cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid
CC   valve disease, angina pectoris, myocardial infarction, cardiac
CC   arrhythmia, pulmonary hypertension, arterial hypertension, renovascular
CC   hypertension, arteriosclerosis, atherosclerosis and/or cardiac tumours
XX
SQ   Sequence 649 BP; 197 A; 162 C; 137 G; 153 T; 0 U; 0 Other;

Query Match   50.1%; Score 601; DB 3; Length 649;
Best Local Similarity   99.7%; Pred. No. 7.5e-142;
Matches 623; Conservative   0; Mismatches   0; Indels   0; Gaps   2;

```
Qy     1  GGAACTAAAAAGAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649  GGAACTAAAAAGAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy    61  AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
                 ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   589  AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy   121  TTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG  180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529  TTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy   181  GCAGATTCCTTAAGCACCCTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
                 ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   469  GCAGATTCCTTAAGCACCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy   241  TCTGCCTACTCTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410  TCTGCCTACTCTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 351

Qy   301  GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350  GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy   361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 231

Qy   421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTTCCATGGCGTGTTCCTTTATCCCCA 480
                 ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   230  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTTCCATGGCGTGTTCCTTTATCCCCA 171

Qy   481  GCGAATTTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT 540
                 |||||||||||||||||||||||||||||||||||||||||||||||
Db   170  GCGAATTTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT 111

Qy   541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGACGCGTGGGCGAGCGAG 600
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   110  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGACGCGTGGGCGAGCGAG  52

Qy   601  CTGGACGCGGGGCGGAGAGGCGGAGC 625
                 ||||||||||||||||||||||||||
Db    51  CTGGACGCGGGGCGGAGAGGCGGAGC  27
```

RESULT 9
ABN95852/c
ID   ABN95852 standard; DNA; 649 BP.

```
XX
AC   ABN95852;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Gene #2350 used to diagnose liver cancer.
XX
KW   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW   metastatic liver tumour; cytostatic; expression profile; disease state;
KW   disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS   Homo sapiens.
XX
PN   WO200229103-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030589.
XX
PR   02-OCT-2000; 2000US-0237054P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Horne D,  Alvares C,  Peres-Da-Silva S,  Vockley JG;
XX
DR   WPI; 2002-426119/45.
XX
PT   Diagnosing and detecting the progression of liver cancer, hepatocellular
PT   carcinoma or metastatic liver tumor in a patient, involves detecting the
PT   level of expression of two or more genes in a liver tissue sample.
XX
PS   Claim 1; SEQ ID NO 2350; 298pp; English.
XX
CC   The invention relates to a novel method for diagnosing and detecting the
CC   progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC   tumour in a patient, and differentiating metastatic liver cancer from
CC   hepatocellular carcinoma in a patient, involving detecting the level of
CC   expression of two or more genes represented in ABN93503-ABN97455 in a
CC   tissue sample. The method of the invention has hepatotropic, and
CC   cytostatic activity. The method is useful for diagnosing and detecting
CC   the progression of liver cancer, hepatocellular carcinoma and metastatic
CC   liver carcinoma in a patient. The method is useful for identifying
CC   expression profiles which serve as useful diagnostic markers as well as
CC   markers that can be used to monitor disease states, disease progression,
CC   drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 649 BP; 197 A; 162 C; 137 G; 153 T; 0 U; 0 Other;

Query Match             50.1%;  Score 601;  DB 6;  Length 649;
Best Local Similarity   99.7%;  Pred. No. 7.5e-142;
Matches  623;       Conservative   0;  Mismatches   0;  Indels   2;  Gaps   2;

Qy          1 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 590

Qy         61 AAGCTTATCTGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTTAGATTTTATT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AAGCTTATCTGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTTAGATTTTATT 530

Qy        121 TTTACATTTGCTAAGTGTCCTAAGTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 TTTACATTTGCTAAGTGTCCTAAGTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy        181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGACGAACTGCTCATT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 GCAGATTCCTTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGACGAACTGCTCATT 411

Qy        241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        410 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 351
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        301 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACTTTGCCATCTCTACACTGG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy        361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTTGATTTTCCAAAAATCCA 231

Qy        421 GGGAACTCCTTTTCCATGAGTACTCCAGGTCCTCCTTGTAAGTAGCCTTTATCCCCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GGGAACTCCTTTTCCATGAGTACTCCAGGTCCTCCTTGTAAGTAGCCTTTATCCCCA 171

Qy        481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTGAGATGGCATT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTGAGATGGCATT 111

Qy        541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGGCGCGGGACCGCTGGGCGAGCTGGGCGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGGCGCGGGACCGCTGGGCGAGCTGGGCGGAG 52

Qy        601 CTGGACGCGGGGCGGGAGAGGCGAGC 625
              ||||||||||||||||||||||||||
Db         51 CTGGACGCGGGGCGGGAGAGGCGAGC 27
```

RESULT 10
ADD18599/c
```
ID   ADD18599 standard; DNA; 649 BP.
XX
AC   ADD18599;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human disease related protein DNA sequence SeqID30.
XX
KW   human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW   antiarteriosclerotic; vulnerary; gene therapy;
KW   hypoxia-regulated condition; tumourigenesis; angiogenesis; apoptosis;
KW   inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW   glucose transportation; catecholamine synthesis; iron transport;
KW   nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW   retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW   inflammatory condition; wound healing; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003018621-A2.
XX
PD   06-MAR-2003.
XX
PF   23-AUG-2002; 2002WO-GB003892.
XX
PR   23-AUG-2001; 2001GB-00020558.
PR   05-OCT-2001; 2001GB-00024037.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  White J,  Ward NR,  Harris RA,  Naylor S,  Mundy CR;
XX
DR   WPI; 2003-290046/28.
DR   P-PSDB; ADD18598.
XX
PT   New substantially purified polypeptide, useful for diagnosing or treating
PT   a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT   injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT   wound healing.
XX
PS   Claim 27; SEQ ID NO 30; 424pp; English.
XX
CC   This invention relates to novel human genes and gene product which are
CC   implicated in certain disease states. Compounds which modulate the
```

CC   proteins of the invention may have cytostatic, antiinflammatory,
CC   ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC   sequences of the invention may be useful for gene therapy. The invention
CC   may be useful for diagnosing or treating a hypoxia-regulated condition,
CC   such as tumourigenesis, angiogenesis, apoptosis, inflammation,
CC   erythropoiesis, or the biological response to hypoxia conditions
CC   including processes such as glycolysis, gluconeogenesis, glucose
CC   transportation, catecholamine synthesis, iron transport or nitric oxide
CC   synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC   injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC   inflammatory conditions or wound healing. The present sequence is that of
CC   a disease related protein encoding DNA sequence of the invention.
XX
SQ   Sequence 649 BP; 197 A; 162 C; 137 G; 153 T; 0 U; 0 Other;

Query Match   50.1%; Score 601; DB 10; Length 649;
Best Local Similarity   99.7%; Pred. No. 7.5e-142;
Matches   623; Conservative   0; Mismatches   0; Indels   2; Gaps   2;

Qy   1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTTGTGTCATGAGAGTTAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTTGTGTCATGAGAGTTAGATTTTATT 530

Qy   121 TTTACATTTGCTAAGTGTCCTGATCGTCCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 TTTACATTTGCTAAGTGTCCTGATCGTCCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 470

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 GCAGATTCCTTAAGCGACCCCTTT-GGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT 411

Qy   241 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 351

Qy   301 GTGGAGGCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 GTGGAGGCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 291

Qy   361 TCCAGGTCCTTCATTATTTTGTCCCAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 TCCAGGTCCTTCATTATTTTGTCCCAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 231

RESULT 11
ADF81436/c
ID   ADF81436 standard; DNA; 649 BP.
XX
AC   ADF81436;
XX
DT   26-FEB-2004 (first entry)
XX
DE   Leukaemia-related DNA sequence #1992.

```
Qy    421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230  GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  171

Qy    481  GCGAATTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT  540
                ||||||||||||||||||||||||||||||||||||||||||||
Db    170  GCGAATTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT  111

Qy    541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGCGGGGACGCTGGGCGAGCTGGGCGAG  600
                |||||||||||||||||||| |||||||||||||||||||||||
Db    110  TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGGGGACGCTGGGCGAGCTGGGCGAG  52

Qy    601  CTGGACGCGGGGCGGGGAGGGCGAGC  625
                |||||||||||||||||||||||
Db    51   CTGGACGCGGGGCGGGGAGGGCGAGC  27
```

RESULT 12
ABX13104/c
ID   ABX13104 standard; cDNA; 649 BP.
XX
AC   ABX13104;
XX
DT   10-MAY-2003 (first entry)
XX
DE   Human cDNA encoding small calcium binding protein p11.
XX
KW   Human; ss; gene; voltage gated sodium channel; VGSC; Nav1.8; p11;
KW   small calcium binding protein; analgesia; chronic pain; osteoarthritis;
KW   rheumatoid arthritis; neuropathic pain; cancer pain;
KW   tri geminal neuralgia; hyperalgesia; inflammatory pain; nociceptive pain;
KW   tabes dorsalis; phantom limb pain; spinal cord injury pain; central pain;
KW   post-herpetic pain; HIV pain; non-cardiac chest pain;
KW   irritable bowel syndrome; bowel disorder.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   112..405
FT   /tag= a
FT   /product= "p11"
XX
PN   WO2003016917-A2.
XX
PD   27-FEB-2003.
XX
PF   20-AUG-2002; 2002WO-GB003852.
XX
PR   20-AUG-2001; 2001GB-00020238.
XX
PA   (UNLO) UNIV COLLEGE LONDON.
XX
PI   Okuse K, Baker M, Poon L, Wood JN, Malik-Hall M;
XX
DR   WPI; 2003-278589/27.
DR   P-PSDB; ABG76194.
XX
PT   Identifying a voltage gated sodium channel (VGSC) modulator for producing
PT   analgesia and for relieving chronic pain, e.g. osteoarthritis or HIV
PT   pain, comprises bringing into contact a VGSC, a p11 peptide and a test
PT   compound.
XX
PS   Disclosure; Page 102-103; 114pp; English.
XX
CC   The invention relates to identifying a modulator of a voltage gated
CC   sodium channel (VGSC) e.g. Nav1.8 comprising: (a) bringing into contact a
CC   VGSC, a p11 peptide (a small calcium binding protein of the S-100 family)
CC   and test compound (tc) so that the VGSC and the p11 peptide can form a
CC   complex in the absence of the (tc); and (b) measuring an activity of the
CC   VGSC, where a change in the activity of the VGSC relative to the activity
CC   in the absence of the (tc) indicates that the (tc) is a modulator of
CC   VGSC. Also included are a method of enhancing the functional expression
CC   of a VGSC in a cell by increasing the level of p11 in the cell, a
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CC   compound identified by a method above, a host cell capable of expressing
CC   a VGSC and a p11 peptide (where the VGSC and/or peptide 11 is expressed
CC   from one or more heterologous expression vectors within the cell),
CC   treating a disorder or condition associated with the activity of a
CC   voltage gated sodium channel (by administering to an individual a
CC   compound identified by the method above, or an inhibitor of p11 activity
CC   or expression). The method is useful for identifying modulators of VGSC.
CC   Compounds identified as modulator of VGSC are useful for manufacturing a
CC   medicament for modulating the functional expression of a voltage gated
CC   sodium channel, for producing analgesia and for relieving chronic pain
CC   such as osteoarthritis, rheumatoid arthritis, neuropathic pain, cancer
CC   pain, tri geminal neuralgia, primary and secondary hyperalgesia,
CC   inflammatory pain, nociceptive pain, tabes dorsalis, phantom limb pain,
CC   spinal cord injury pain, central pain, post-herpetic pain and HIV pain,
CC   non-cardiac chest pain, irritable bowel syndrome and pain associated with
CC   bowel disorders. The present sequence encodes human p11
XX
SQ   Sequence 649 BP; 197 A; 162 C; 153 T; 0 U; 0 Other;

Query Match             50.1%;  Score 601;  DB 10;  Length 649;
Best Local Similarity   99.7%;  Pred. No. 7.5e-142;
Matches  623;  Conservative   0;  Mismatches   0;  Indels   2;  Gaps   2;

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Qy     1  GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACATACAAAAATCAA  60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649  GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACATACAAAAATCAA  590

Qy    61  AAGCTTTATCTGGTATTTAACTTTCTTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589  AAGCTTTATCTGGTATTTAACTTTCTTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT  530

Qy   121  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGG  180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGG  470

Qy   181  GCAGATTCCTTAAGCACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  240
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   469  GCAGATTCCTTAAGCACCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  411

Qy   241  TCTGCCTACTTCTTCCCTTCTCGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410  TCTGCCTACTTCTTCCCTTCTCGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATG  351

Qy   301  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG  360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG  291

Qy   361  TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTCTTTTGATTTTCCAAAAATCCA  420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290  TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTCTTTTGATTTTCCAAAAATCCA  231

Qy   421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230  GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA  171

Qy   481  GCGAATTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT  540
             |||||||||||||||||||||||||||||||||||||||||||||
Db   170  GCGAATTGTGAAATGTAAACATCATGGTTCCATTTGAGATGGCATT  111

Qy   541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGCGGGGACGCTGGGCGGAG  600
             ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   110  TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGGGGACGCTGGGCGAGCTGGGCGAG  52

Qy   601  CTGGACGCGGGGCGGGGAGGGCGAGC  625
             |||||||||||||||||||||||||
Db    51  CTGGACGCGGGGCGGGGAGGGCGAGC  27
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RESULT 13
ADR24986/c
ID   ADR24986 standard; DNA; 649 BP.
XX
AC   ADR24986;

```
XX
DT   21-OCT-2004   (first entry)
XX
DE   Breast cancer prognosis marker #847.
XX
KW   ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2004065545-A2.
XX
PD   05-AUG-2004.
XX
PF   15-JAN-2004; 2004WO-US001100.
XX
PR   15-JAN-2003; 2003US-00342887.
XX
PA   (ROSE-) ROSETTA INPHARMATICS LLC.
PA   (NECA-) NETHERLANDS CANCER INST.
XX
PI   Van't Veer LJ, He Y;
XX
DR   WPI; 2004-593473/57.
XX
PT   Classifying a breast cancer patient according to prognosis comprises
PT   determining the similarity between the level of expression of each of
PT   five genes in a cell sample taken from patient, to control levels.
XX
PS   Disclosure; SEQ ID NO 847; 226pp; English.
XX
CC   The invention relates to a method of classifying a breast cancer patient
CC   according to prognosis by determining the similarity between the level of
CC   expression of each of five genes for which markers are listed in the
CC   specification, in a cell sample taken from the breast cancer patient, to
CC   control levels of expression for each respective five genes to obtain a
CC   patient similarity value. The methods are useful for classifying a breast
CC   cancer patient according to prognosis. Kits and computer program products
CC   are useful for data analysis using the diagnostic, prognostic and
CC   statistical methods of the invention. This sequence corresponds to a
CC   marker used in the method of the invention.
XX
SQ   Sequence 649 BP; 197 A; 162 C; 137 G; 153 T; 0 U; 0 Other;

Query Match             50.1%;  Score 601;  DB 13;  Length 649;
Best Local Similarity   99.7%;  Pred. No. 7.5e-142;
Matches   623;  Conservative   0;  Mismatches   0;  Indels   2;  Gaps   2;

Qy        1 GGAACTCAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      649 GGAACTCAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy       61 AAGCTTATCTGGTATTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      589 AAGCTTATCTGGTATTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy      121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTCTGATGGGGAAGCTGTGGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTCTGATGGGGAAGCTGTGGG 470

Qy      181 GCAGATTCCTCAAGCGACCCTTGGGACAACTCCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      469 GCAGATTCCTCAAGCGACCCCTTT-GGACAACTCCTTATCAGGGAGGAGGAGCGAACTGCTCATT 411

Qy      241 TCTGCCTACTTCTTTCCCTTCCGCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      410 TCTGCCTACTTCTTTCCCTTCCGCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 351

Qy      301 GTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      350 GTGAGGCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy      361 TCCAGGTCCTTCATTATTTGTTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      290 TCCAGGTCCTTCATTATTTGTTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCCA 231

Qy      421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      230 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCA 171

Qy      481 GCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 540
            |||||||||||||||||||||||||||||||||||||||||||||
Db      170 GCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 111

Qy      541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGGCGGCGACGCTGGGCGAGCTGGGCGAG 600
            ||||||||||||||||||||| |||| ||||||||||||||||| |||||||||||||||
Db      110 TTGGTGTGGTCCGTTGAAGCCCTTGG-CGAGGGCGGCGGCGACCTGGGCGGCGAGCTGGGCGAG 52

Qy      601 CTGGACGCGGGGCGCGGAGAGGCGAGC 625
            |||||||||||| ||||||||||||||
Db       51 CTGGACGCGGGGGCGGAGAGGCGAGC 27


RESULT 14
ADP54125/c
ID   ADP54125 standard; cDNA; 649 BP.
XX
AC   ADP54125;
XX
DT   18-NOV-2004   (first entry)
XX
DE   Human PRO cDNA sequence SEQ ID NO:101.
XX
KW   human; PRO; immune related disease; inflammatory immune response;
KW   immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW   antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW   antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW   haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW   nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW   virucide; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200039956-A2.
XX
PD   13-MAY-2004.
XX
PF   28-OCT-2003; 2003WO-US034381.
XX
PR   29-OCT-2002; 2002US-0422472P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI   Wood WI, Wu TD;
XX
DR   WPI; 2004-376182/35.
DR   P-PSDB; ADP54126.
XX
PT   New PRO polynucleotides and polypeptides, useful in useful in diagnosing
PT   and treating an immune related disease, e.g. systemic lupus
PT   erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT   stimulating an immune response.
XX
PS   Claim 2; SEQ ID NO 101; 3009pp; English.
XX
CC   The present invention describes an isolated PRO nucleic acid (I). Also
CC   described: (1) a vector comprising (I); (2) a host cell comprising the
CC   vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC   isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC   polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC   antibody which specifically binds to a polypeptide of (4); (7) a
CC   composition of matter comprising a polypeptide of (4), an agonist or
CC   antagonist of the polypeptide or an antibody that binds to the
CC   polypeptide in combination with a carrier; (8) an article of manufacture
CC   comprising a container, a label on the container and a composition of
CC   matter of (7); (9) a method of treating an immune related disease in a
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CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC ; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO nucleotide sequence from the present invention.
XX
SQ Sequence 649 BP; 197 A; 162 C; 137 G; 153 T; 0 U; 0 Other;

Query Match   50.1%; Score 601; DB 13; Length 649;
Best Local Similarity   99.7%; Pred. No. 7.5e-142;
Matches   623; Conservative   0; Mismatches   0; Indels   0; Gaps   2;

Qy   1 GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 649 GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 589 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy 121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 470

Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
         |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db 469 GCAGATTCCTTAAGCGACCCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy 241 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 410 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 351

Qy 301 GTGAGGGCCCGCAATTAGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 350 GTGAGGGCCCGCAATTAGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy 361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 290 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 231

Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCAGGTCCTTGTTAAGTAGCCTTATCCCCA 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 230 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCAGGTCCTTGTTAAGTAGCCTTATCCCCA 171

Qy 481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAATGGCATT 540
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 170 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAATGGCATT 111

Qy 541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGACGCTGGGCGGGGAG 600
         ||||||||||||||||||||||||| |
Db 110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGGCGGAGCTGGGCGAGCTGGGGCGGAG 52

Qy 601 CTTGGACCGGCGGGGCGGGAGGAGGCGAGC 625
         ||||||||||||||||||||||||||||||
Db   51 CTTGGACCGGCGGGGCGGGAGGAGGCGAGC 27

RESULT 15
ADS17592/c
ID ADS17592 standard; cDNA; 649 BP.
XX
AC ADS17592;

XX
DT 16-DEC-2004 (first entry)
XX
DE Nucleotide sequence of the p11 subunit of human annexin II.
XX
KW neurite outgrowth; neuronal cell; annexin II; neurodegeneration;
KW Alzheimer's disease; Parkinsonian syndrome; brain injury; stroke;
KW p11 subunit; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   112..405
FT   /*tag= a
FT   /product= "p11 subunit of human annexin II"
XX
PN WO2004080424-A2.
XX
PD 23-SEP-2004.
XX
PF 13-MAR-2004; 2004WO-US007749.
XX
PR 13-MAR-2003; 2003US-0454254P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Yeh L, Cuny GD, Padmanaban D, Ding K;
XX
DR WPI; 2004-668882/65.
DR P-PSDB; ADS17593.
XX
PT Determining neurite outgrowth in a population of neuronal cells comprises
PT detecting the amount of annexin II in the population of neuronal cells.
XX
PS Disclosure; SEQ ID NO 3; 67pp; English.
XX
CC The specification describes a method for quantitatively determining
CC neurite outgrowth in a population of neuronal cells. The method comprises
CC contacting a population of neuronal cells with a detection reagent
CC capable of detecting annexin II, detecting an amount of annexin II in the
CC population of neuronal cells, and determining a quantitative amount of
CC neurite outgrowth in the population of neuronal cells based on the amount
CC of annexin II. The method is useful for detecting neurite outgrowth and
CC for screening compounds that modulate neurite outgrowth or that may be
CC used to prevent or treat diseases and conditions relating to
CC neurodegeneration, such as Alzheimer's disease, Parkinsonian syndromes,
CC brain injuries or stroke. The present sequence encodes the p11 subunit of
CC human annexin II. The p11 nucleotide sequence can be detected using the
CC method of the invention.
XX
SQ Sequence 649 BP; 197 A; 162 C; 137 G; 153 T; 0 U; 0 Other;

Query Match   50.1%; Score 601; DB 13; Length 649;
Best Local Similarity   99.7%; Pred. No. 7.5e-142;
Matches   623; Conservative   0; Mismatches   0; Indels   0; Gaps   2;

Qy   1 GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 649 GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 590

Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 589 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530

Qy 121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 529 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 470

Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
         |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db 469 GCAGATTCCTTAAGCGACCCCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 411

Qy 241 TCTGCCTACTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents cDNA encoding a human ovarian antigen of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 663 BP; 213 A; 148 C; 144 G; 152 T; 0 U; 6 Other;

Query Match   49.7%; Score 595.8; DB 6; Length 663;
Best Local Similarity   99.5%; Pred. No. 1.6e-140;
Matches 597;   Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   2 GAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAAA 61
               ||||||||||||||||||||||||||||||||| ||| ||||||||||||||| |||||||
Db   601 GAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAACCAATNCAAAAAATCAAA 542

Qy   62 AGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTT 121
               ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   541 AGCTTATCTGGTATTTAACTTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTT 482

Qy   122 TTACATTTGCTAAGTGCCGATCGTCCTGCTCATGAAATCCTTCATGGGGAAGCGTGTGGGG 181
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTACATTTGCTAAGTGCCGATCGTCCTGCTCATGAAATCCTTCATGGGGAAGCGTGTGGGG 422

Qy   182 CAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTT 241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAGATTCCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTT 362

Qy   242 CTGCCTACTTCTTCCCTTCTGCTTCGTCTGCTTGTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATGG 301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CTGCCTACTTCTTCCCTTCTGCTTCGTCTGCTTGTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATGG 302

Qy   302 TGAGGCCCGCAATTAGGAGAAAAGAAGTCTCGGAAGCCCACTTTGCCATCTCTACACTGGT 361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGAGGCCCGCAATTAGGAGAAAAGAAGTCTCGGAAGCCCACTTTGCCATCTCTACACTGGT 242

Qy   362 CCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAG 421
               |||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||
Db   241 CCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAG 182

Qy   422 GGAACTCCTTTTCCATGAGTACTCCCAGGTCCTCCAGGTCCTCCAGGTCCTCCAGGTCCTTTATCCCCAG 481
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGAACTCCTTTTCCATGAGTACTCCCAGGTCCTCCAGGTCCTCCAGGTCCTTTATCCCCAG 122

Qy   482 CGAATTTGTGAAATGTAAACATCATGTTTCCATTGAGATGGCATTT 541
               ||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGAATTTGTGAAATGTAAACATCATGTTTCCATTGAGATGGCATTT 62

Qy   542 TGGTGTGGTCCGTTGAAGCCTTGAAGCGCTGGGCGGACGCGCTGGGCGGAGC 601
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   51 CTGGACGCGCGGGGCGGGAGGAGGCGAGC 27

Db   410 TCTGCCTACTTCTTCCCTTCTGCTTCGTCTGCTTGTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 351
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 GTGAGGCCCGCAATTAGGAGAAAAGAAGTCTCGGAAGCCCACTTTGCCATCTCTACACTGG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 GTGAGGCCCGCAATTAGGAGAAAAGAAGTCTCGGAAGCCCACTTTGCCATCTCTACACTGG 291

Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 231

Qy   421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 480
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 171

Qy   481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGCGTGTTCCATTGAGATGGCATT 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   170 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGCGTGTTCCATTGAGATGGCATT 111

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGCCGAGGCGCGCGGACGGCTGGGCGAGCGCGGCGGAG 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   110 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGCGCGGCGGACGGCTGGGCGAGCGCGGCGGAG 52

Qy   601 CTGGACGCGCGGGGCGGGAGGAGGCGAGC 625
               |||||||||||||||||||||||||||||
Db   51 CTGGACGCGCGGGGCGGGAGGAGGCGAGC 27

RESULT 16
ABQ55234/c
ID ABQ55234 standard; cDNA; 663 BP.
XX
AC ABQ55234;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HCOOI71 cDNA, SEQ ID NO:1114.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US018569.
XX
PR 07-JUN-2000; 2000US-0209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR P-PSDB; ABP42157.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX
PS Claim 1; SEQ ID NO 1114; 2922pp; English.
XX

```
Db    61 TGGTGTGGTCCGTTGAAGCCTTGGCCCGAGGGCCGGCGGACGCTGGGCCGAGCTGGGCCGAGC  2
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 17
AAA46667/c
ID    AAA46667 standard; cDNA; 579 BP.
XX
AC    AAA46667;
XX
DT    25-SEP-2000  (first entry)
XX
DE    cDNA of a human gene encoding cellular ligand of annexin II.
XX
KW    Differentially expressed human gene; cardiac disease; kidney disease;
KW    inflammatory disease; I-8U; prostacyclin-stimulating factor; isf-2;
KW    tissue specific mRNA; insulin-like growth factor binding protein 6;
KW    OSF-1; gas-1; YMP; BTG2; pre-B cell stimulating factor homologue; SDF1a;
KW    peripheral benzodiazepine receptor; annexin II cellular ligand; pll;
KW    congenital heart failure; dilated congestive cardiomyopathy;
KW    hypertrophic cardiomyopathy; restrictive cardiomyopathy;
KW    mitral valve disease; aortic valve disease; tricuspid valve disease;
KW    angina pectoris; myocardial infarction; cardiac arrhythmia;
KW    pulmonary hypertension; arterial hypertension; renovascular hypertension;
KW    arteriosclerosis; atherosclerosis; cardiac tumour; ss.
XX
OS    Homo sapiens.
XX
PN    WO200035473-A2.
XX
PD    22-JUN-2000.
XX
PF    15-DEC-1999;  99WO-US029941.
XX
PR    18-DEC-1998;  98US-0113008P.
XX
PA    (SCIO-) SCIOS INC.
XX
PI    Stanton LW, White RT, Damm DL, Lewicki JA, Joly A, Schreiner GF;
XX
DR    WPI; 2000-451904/39.
XX
PT    Preventing, diagnosing and treating cardiac, kidney and inflammatory
PT    disorders using cardiac genes that are differentially expressed in
PT    disease states such as cardiac arrhythmia and arteriosclerosis.
XX
PT    Disclosure; Fig 5L; 170pp; English.
XX
CC    AAA46656-67 represent differentially expressed human genes, associated
CC    with disease states and disorders. The specification describes methods
CC    preventing, diagnosing and treating cardiac, kidney and inflammatory
CC    diseases associated with inappropriate expression of differentially
CC    expressed cardiac, kidney and inflammatory genes (e.g. AAA46656-67).
CC    These genes include I-8U, prostacyclin-stimulating factor, isf-2, tissue
CC    specific mRNA, insulin-like growth factor binding protein 6, OSF-1, gas-
CC    1, YMP, BTG2, pre-B cell stimulating factor homologue (SDF1a), peripheral
CC    benzodiazepine receptor, and cellular ligand of annexin II (pll),
CC    respectively. These diseases include congenital heart failure, dilated
CC    congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive
CC    cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid
CC    valve disease, angina pectoris, myocardial infarction, cardiac
CC    arrhythmia, pulmonary hypertension, arterial hypertension, renovascular
CC    hypertension, arteriosclerosis, atherosclerosis and/or cardiac tumours
XX
SQ    Sequence 579 BP; 185 A; 127 C; 124 G; 143 T; 0 U; 0 Other;

Query Match    46.5%;  Score 557;  DB 3;  Length 579;
Best Local Similarity  99.7%;  Pred. No. 1e-130;
Matches  579;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy     1 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   579 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  520
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Qy    61 AAGCTTATCTGGTATTAAACTTTTCTTTTCTCTGCTGTGTCAAATGAGAGTTAGATTTTATT  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   519 AAGCTTATCTGGTATTAAACTTTTCTTTTCTCTGCTGTGTCAAATGAGAGTTAGATTTTTATT  460

Qy   121 TTTACATTTGCTAAGTGTCCTAAGTGTCCTGATCTGCTGTGTCAAATCCTTCATGGGGAAGCTGTGTGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   459 TTTACATTTGCTAAGTGTCCTGATCTGCTGTCATGAAATCCTTCATGGGGAAGCTGTGTGG  400

Qy   181 GCAGATTCCTAAGGCAACCCTTGGACAACTCTTATCAGGGAGGAGGCGGAACTGCTCATT  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   399 GCAGATTCCTAAGGCACCCTTT-GGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT  341

Qy   241 TCTGCCTACTCTTCCCTTCGCTTCATGTGTACACAAAATAGTCATTGCATGCAATG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   340 TCTGCCTACTCTTCCCTTCGCTTCATGTGTACACAAAATAGTCATTGCATGCAATG  281

Qy   301 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   280 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG  221

Qy   361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   220 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA  161

Qy   421 GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTGTAAGTAGCCTTTATCCCCA  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   160 GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTGTAAGTAGCCTTTATCCCCA  101

Qy   481 GCGAATTGTGAAATGTAAACATCATGTTTCCATTGGATGGCATT  540
         ||||||||||||||||||||||||||||||||||||||||||||
Db   100 GCGAATTGTGAAATGTAAACATCATGTTTCCATTGGATGGCATT  41

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGCGGGGAC  581
         |||||||||||||||||||||||||||||||||||||||||
Db    40 TTGGTGTGGTCCGTTGAAGCCTTGG-CGAGGGCGCGGGGAC  1
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RESULT 18
ABK45339
ID    ABK45339 standard; cDNA; 571 BP.
XX
AC    ABK45339;
XX
DT    05-JUN-2002  (first entry)
XX
DE    cDNA encoding colon tumour protein, SEQ ID No 890.
XX
KW    Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
KW    gene; ss.
XX
OS    Homo sapiens.
XX
PN    WO200212328-A2.
XX
PD    14-FEB-2002.
XX
PF    31-JUL-2001;  2001WO-US024218.
XX
PR    03-AUG-2000;  2000US-0223283P.
PR    28-MAR-2001;  2001US-0279763P.
PR    29-JUN-2001;  2001US-0302051P.
XX
PA    (CORI-) CORIXA CORP.
XX
PI    King GE, Meagher MJ, Xu J,   Secrist H;
XX
DR    WPI; 2002-241739/29.
XX
PT    New colon cancer polypeptides and polynucleotides, useful as vaccines,
PT    for diagnosing, preventing, and treating colon cancer, and as markers for
PT    the progression of cancer.
XX
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PS  Claim 1; SEQ ID NO 890; 147pp; English.
XX
CC  The invention relates to polynucleotides encoding colon tumour proteins.
CC  The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC  compositions, such as vaccines, for the diagnosis, prevention, and
CC  treatment of colon cancer. Polynucleotide sequences may be used as
CC  hybridisation probes or primers, and in the design and preparation of
CC  ribozyme molecules for inhibiting expression of tumour polypeptides and
CC  proteins in tumour cells. The compositions are useful for stimulating an
CC  immune response against cancer, particularly for the immunotherapy of
CC  colon cancer, and as markers for the progression of cancer. ABK46237
CC  ABK46237 represent coding sequences of human colon tumour proteins of the
CC  invention. Note: With the exception of SEQ ID No 1 and 2, the sequence
CC  data for this patent did not form part of the printed specification but
CC  was supplied by the European Patent Office
XX
SQ  Sequence 571 BP; 139 A; 115 C; 107 G; 203 T; 0 U; 7 Other;

Query Match             44.8%;  Score 537;  DB 6;  Length 571;
Best Local Similarity   98.7%;  Pred. No. 1.2e-125;
Matches   537;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   28 GNAACTAAAAAANAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 87

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   88 AAGCTTATCTGGTATTTAACTTTCTTCTCTCGCTTGTCAAATGAGAGTTANATTTTATT 147

Qy  121 TTTACATTGCTAAGTGTCCTGATCGTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148 TTTACATTGCTAAGTGTCCTGATCGTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 207

Qy  181 GCAGATTCCTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  208 GCANATTCCTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 267

Qy  241 TCTGCCTACTTCTTTCCCTTGCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  268 TCTGCCTACTTCTTTCCCTTGCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 327

Qy  301 GTGAGGGCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCCTCACACTGG 360
          |||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  328 GTGAGGGCCCGCAATTAGGGAAAANAGCTCTGGAAGCCCACTTTGCCATCCTCACACTGG 387

Qy  361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  388 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 447

Qy  421 GGGAACTCCTTTCCATGAGTACTCCTCAGGTCCTTAAGTAGCCTTTATCCCCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  448 GGGAACTCCTTTCCATGAGTACTCCTCAGGTCCTTAAGTAGCCTTTATCCCCA 507

Qy  481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 540
          ||||||| |||||||||||||||||||||||||||||| |||||||
Db  508 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGANATGGCATT 567

Qy  541 TTGG 544
          ||||
Db  568 TTGG 571

RESULT 19
AAC10823/c
ID   AAC10823 standard; cDNA; 582 BP.
XX
AC   AAC10823;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 14898.
XX
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KW  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW  gene therapy; chromosome mapping; ss.
XX
OS  Homo sapiens.
XX
PN  EP1033401-A2.
XX
PD  06-SEP-2000.
XX
PF  21-FEB-2000; 2000EP-00200610.
XX
PR  26-FEB-1999;  99US-0122487P.
XX
PA  (GEST ) GENSET.
XX
PI  Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR  WPI; 2000-500381/45.
XX
PT  New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT  obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT  diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS  Claim 1; SEQ ID NO 14898; 71pp + Sequence Listing; English.
XX
CC  The present sequence is one of a large number of 5' ESTs derived from
CC  mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC  identified within the present sequence. The 5' ESTs were prepared from
CC  total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC  sequences usually correspond mainly to the 3' untranslated region (UTR)
CC  of the mRNA because they are often obtained from oligo-dT primed cDNA
CC  libraries. Such ESTs are not well suited for isolating cDNA sequences
CC  derived from the 5' ends of mRNAs and even in those cases where longer
CC  cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC  ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC  to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC  diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC  They are used to obtain upstream regulatory sequences and to design
CC  expression and secretion vectors
XX
SQ  Sequence 582 BP; 183 A; 135 C; 130 G; 129 T; 0 U; 5 Other;

Query Match             43.6%;  Score 523;  DB 3;  Length 582;
Best Local Similarity   97.9%;  Pred. No. 4.1e-122;
Matches   547;  Conservative    4;  Mismatches    4;  Indels    4;  Gaps    2;

Qy   30 GGCAAGGGATGCAAACAATACAAAAATCAAAAGCTTATCTGGTATTTAACTTTCTTC 89
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  582 GGCAAGGGATCCAAACAATACAAAAATCAAAAGCTTATCTGGTATTTAACTTTCTTC 523

Qy   90 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTGGTCCTGATCGTGCT 149
          |||||||||||||||||||||||||||||||||||||| |||||||||||||
Db  522 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTGCTCCTGATCGTGCT 463

Qy  150 CATGAAATCCTTCTATGGGGGAAGCTCGTGGGGCAGATTCCTAAGCGACCCTTTGGGACA 209
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||  ||||
Db  462 CATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATTCCTAAGCGACCCTTT--GACA 405

Qy  210 ACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTCTTTCTGCCTACTTCTTTCTGCTTCAT 269
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  404 ACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCCTACTTCTTTCTGCCTACTTCTTTCTGCTTCAT 345

Qy  270 GTGTACTACAAAAATAGTCATTGCATGCAATGTGAGGGCCCGCAATTAGGGAAAAGAAGCT 329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  344 GTGTACTACAAAAATAGTCATTGCATGCAATGTGAGGGCCCGCAATTAGGGAAAAGAAGCT 285

Qy  330 CTGGAAGCCCACTTTGCCATCTCACACTGGTCCTTCATTATTTTGTCCACAGC 389
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  284 CTGGAAGCCCACTTTGCCATCTCACACTGGTCCTTCATTATTTTGTCCACAGC 225

Qy  390 CAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCAGGGAACTCCTCAG 449
          |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db  224 CAGAGGGTC--TTTGATTTTCCAAAAATCCAGGGAACTCCAGGGAACTCCTCAG 167
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Qy  450 GTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGGCGAATTTGTGAAATGTAAACATCATGGT 509
            ||||||||||||||||||||||||||| |||||||::||::||::||||||||||||||
Db  166 GTCCTCCTTTGTTAAGTAGCCTTTATYCCCAGCGAATTTGYGAAATGTAMACRTCATGGT 107

Qy  510 TTCCATGGCGTGTCCATTTGAGATGGCATTTGGTGTGGTCCGGTTGAAGCCTTGGCGGA 569
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  106 TTCCATGGCGTGTCCATTTGAGATGGCATTTGGTGTGGTCCGGTTGAAGCCTTGGCCGA 47

Qy  570 GGGCGGCGGCGACGCTGGGC 588
            ||||||| | |   ||
Db  46  GGCGCGCGGGGGCTGTCGC 28

RESULT 20
ADK11670/c
ID   ADK11670 standard; DNA; 530 BP.
XX
AC   ADK11670;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Breast cancer differentially expressed gene product #76.
XX
KW   ds; cytostatic; gene therapy; DKFZp561I133 activity inhibitor;
KW   breast cancer; differential expression.
XX
OS   Homo sapiens.
XX
PN   WO200305926-A1.
XX
PD   17-JUL-2003.
XX
PF   08-JAN-2003; 2003WO-US000657.
XX
PR   08-JAN-2002; 2002US-0345637P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Hansen R;
XX
DR   WPI; 2003-577534/54.
XX
PT   Inhibiting a cancerous phenotype of a cell, useful for treating breast
PT   cancer comprises contacting a cancerous mammalian cell with an agent for
PT   inhibition of DKFZp561I133 activity.
XX
PS   Claim 30; SEQ ID NO 76; 257pp; English.
XX
CC   The invention relates to a method of inhibiting a cancerous phenotype of
CC   a cell comprises contacting a cancerous mammalian cell with an agent for
CC   inhibition of DKFZp561I133 activity. The methods are useful for treating
CC   cancer, e.g. breast cancer. This sequence represents a gene product which
CC   is differentially expressed in breast cancer cells. The sequence can be
CC   used in the method of the invention.
XX
SQ   Sequence 530 BP; 160 A; 133 C; 124 G; 113 T; 0 U; 0 Other;

Query Match             43.1%;  Score 516.8;  DB 10;  Length 530;
Best Local Similarity   99.6%;  Pred. No. 1.5e-120;
Matches  518;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy  102 ATGAGAGTTAGATTTATTTTTACATTGCTAAGTGCCTGATCGTGCTCATGAAAATCCTT 161
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  530 ATGAGAGTTAGATTTATTTTTACATTGCTAAGTGTCCTGATCGTGCTCATGAAAATCCTT 471

Qy  162 CTATGGGGGAAGCTGTCGGGGCAGATTCCTTAAGCGACACCCTTGGACAACAACTTATCAGA 221
            ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  470 CTATGGGGGAAGCTGTCGTGGGCAGATTCCTTAAGCGACACCCTTGGACAACAACTTATCAAG 411

Qy  222 GAGGAGGCGAACTGCTCATTTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAA 281
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  410 GAGGAGGCGAACTGCTCATTTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAA 351
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Qy  282 ATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCAC 341
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  350 ATAGTCATTACATGCAATGGTGAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCAC 291

Qy  342 TTTGCCATCTCTACACTGGTCCAGTGCCTTCATTATTTGTCTCAGCCAGAGGGTCTTT 401
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  290 TTTGCCATCTCTACACTGGTCCAGTGCCTTCATTATTTGTCTCAGCCAGAGGGTCTTT 231

Qy  402 TTGATTTTCCAAAAATCCAGGAACTCCTTTTCCATGAGTACTTCCAGTGTCCTTTGT 461
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  230 TTGATTTTCCAAAAATCCAGGAACTCCTTTTCCATGAGTACTTCCAGTGTCCTTTGT 171

Qy  462 TAAGTAGCCTTTATCCCCAGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTG 521
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  170 TAAGTAGCCTTTATCCCCAGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTG 111

Qy  522 TTCCATTTGAGATGGCATTTGGTGTGGTCCGTTGAAGCCTTGGCCGGGCGGCCGAC 581
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  110 TTCCATTTGAGATGGCATTTGGTGTGGTCCGTTGAAGCCTTGGCCGGGCGGCCGAC 51

Qy  582 GCTGGGCGGCGAGCTGGGCGGCGGCGGGGGCCGGAGGC 621
            ||||||||||||||||||||||||||||||||||||
Db  50  GCTGGGCGGCGAGCTGGGCGGCGGCGGGGGCCGGAGGC 11

RESULT 21
ACC51060/c
ID   ACC51060 standard; cDNA; 2016 BP.
XX
AC   ACC51060;
XX
DT   13-JUN-2003  (first entry)
XX
DE   Human S-100A10 Related Protein coding sequence.
XX
KW   Human; GENSET; therapeutic; therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200294864-A2.
XX
PD   28-NOV-2002.
XX
PF   06-AUG-2001; 2001WO-IB001715.
XX
PR   25-MAY-2001; 2001US-0293574P.
PR   15-JUN-2001; 2001US-0298698P.
PR   29-JUN-2001; 2001US-0302277P.
PR   13-JUL-2001; 2001US-0305456P.
XX
PA   (GEST ) GENSET.
XX
PI   Bejanin S, Tanaka H;
XX
DR   WPI; 2003-129412/12.
DR   P-PSDB; ABR48453.
XX
PT   New GENSET polynucleotides and polypeptides, useful for preparing a
PT   composition for treating GENSET-related disorders and as reagents in
PT   assays to quantitatively determined levels of GENSET expression in
PT   biological samples.
XX
PS   Claim 1; Page 400-401; 505pp; English.
XX
CC   The present invention relates to novel human GENSET coding sequences
CC   (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
CC   sequences are useful for preparing a composition for treating GENSET-
CC   related disorders. They can also be used as markers for tissues in which
CC   the corresponding protein is preferentially expressed, as molecular
CC   weight markers on Southern gels, as chromosome markers or tags to
CC   identify chromosomes, and as reagents in assays to quantitatively
CC   determined levels of GENSET expression in biological samples
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PI   Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Claim 1; SEQ ID NO 21508; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 477 BP; 158 A; 100 C; 109 G; 109 T; 0 U; 1 Other;

Query Match   35.8%;   Score 429.4; DB 9;   Length 477;
Best Local Similarity   99.8%;   Pred. No. 1.9e-98;
Matches 430;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   92   TGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCTAAGTGTCCTGATCTGCTCA   151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   477   TGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCTAAGTGTCCTGATCTGCTCA   418

Qy   152   TGAAATCCTTCATGGGGAGCGTGTGGGCAGATTCCTTAAGCGACCCTTTGGGACAAC   211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   417   TGAAATCCTTCATGGGGAGCGTGTGGGCAGATTCCTTAAGCGACCCTTTGGGACAAC   358

Qy   212   TCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGT   271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   357   TCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTGCTTCATGT   298

Qy   272   GTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCT   331
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   297   GTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCT   238

Qy   332   GGAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTAAGCGTCCTCATTATTTTGTCCACAGCCA   391
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   237   GGAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTAAGCGTCCTCATTATTTTGTCCACAGCCA   178

Qy   392   GAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGT   451
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   177   GAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGT   118

Qy   452   CCTCCTTCGTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGTTT   511
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   117   CCTCCTTCGTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGTTT   58

Qy   512   CCATGGCGTGT   522
           |||||||||||
Db   57   CCATGGCGTCT   47

RESULT 23
ADF79487/c
ID   ADF79487 standard; DNA; 434 BP.
XX
AC   ADF79487;

XX
SQ   Sequence 2016 BP; 625 A; 461 C; 428 G; 502 T; 0 U; 0 Other;

Query Match   40.5%;   Score 485.2; DB 8;   Length 2016;
Best Local Similarity   94.7%;   Pred. No. 2.6e-112;
Matches 502;   Conservative   0;   Mismatches   0;   Indels   28;   Gaps   0;

Qy   73   TATTTAACTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCT   132
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2012   TTTTTTTTTTTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCT   1953

Qy   133   AAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAGCGTGTGGGCAGATTCCTTA   192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1952   AAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAGCGTGTGGGCAGATTCCTTA   1893

Qy   193   AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC   252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1892   AGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTC   1833

Qy   253   TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA   312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1832   TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCA   1773

Qy   313   ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTC   372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1772   ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTC   1713

Qy   373   ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT   432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1712   ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT   1653

Qy   433   TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA   492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1652   TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA   1593

Qy   493   AATGTAAACATCATGTTTCCATGGCGTGTTCCATTGAGATGGCATTTTGGTGGTCC   552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1592   AATGTAAACATCATGTTTCCATGGCGTGTTCCATTGAGATGGCATTTTGGTGGTCC   1533

Qy   553   GTTGAAGCCTTGGCCCAGGCGCGGCGACGCTGGGCGAGCT   602
           ||||||||| ||||||||||||| |||| |||
Db   1532   GTTGAAGCCACCAGGCAGAGGCTCAGTGCGCAGGTCGCAGGTCTGGGCAGCCAAGAGAAAAGT   1483

RESULT 22
ACH34296/c
ID   ACH34296 standard; cDNA; 477 BP.
XX
AC   ACH34296;
XX
DT   13-OCT-2003   (first entry)
XX
DE   Human endothelial cell cDNA #2429.
XX
KW   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW   genome mapping; biodiversity; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX

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Qy        486  TTTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGT 545
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75  TTTGTGAAATGTAAACATCATGGTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGT 16

Qy        546  GTGGTCCGTTGAAGC 560
               |||||||||||||||
Db         15  GTGGTCCGTTGAAGC 1
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RESULT 24
ACH25344/c

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ID   ACH25344 standard; cDNA; 466 BP.
XX
AC   ACH25344;
XX
DT   13-OCT-2003   (first entry)
XX
DE   Human adult ovary cDNA #3724.
XX
KW   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW   genome mapping; biodiversity; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT, Labat I,   Stache-Crain B,   Dickson MC,    Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridisation probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Claim 1; SEQ ID NO 12556; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 466 BP; 142 A; 102 C; 108 G; 106 T; 0 U; 8 Other;
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Query Match             35.2%;  Score 422;  DB 9; Length 466;
Best Local Similarity  100.0%;  Pred. No. 1.4e-96;
Matches  422;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

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XX
DT   26-FEB-2004   (first entry)
XX
DE   Leukaemia-related DNA sequence #43.
XX
KW   Cytostatic; Gene therapy; leukaemia; ss.
XX
OS   Unidentified.
XX
PN   WO200303943-A2.
XX
PD   15-MAY-2003.
XX
PF   04-NOV-2002; 2002WO-EP012303.
XX
PR   05-NOV-2001; 2001EP-00126244.
PR   30-APR-2002; 2002EP-00009758.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA   (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA   (HAFE/) HAFERLACH T.
PA   (SCHO/) SCHOCH C.
PA   (KERN/) KERN W.
XX
PI   Haferlach T,  Schoch C,  Kern W,  Kohlmann A,  Schnittger S,   Dugas M;
PI   Eils R,  Brors B,  Mergenthaler S;
XX
DR   WPI; 2003-505037/47.
XX
PT   Determining the subtype of leukaemia cells and whether a patient sample
PT   contains leukemia cells or other cells, useful for treating leukemia,
PT   comprises determining the expression profile of a group of markers in a
PT   patient sample.
XX
PS   Disclosure; SEQ ID NO 43; 293pp; English.
XX
CC   The present invention relates to a method (M1) for determining the
CC   subtype of leukaemia cells and whether a patient sample contains
CC   leukaemia cells. The method comprises determining the expression profile
CC   of a group of markers in a patient sample. The method is useful for
CC   determining the presence of leukaemia cells, its types or subtypes, and
CC   for the preparation of a medicament for treating leukaemia.
XX
SQ   Sequence 434 BP; 139 A; 96 C; 102 G; 97 T; 0 U; 0 Other;
```

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Query Match             35.3%;  Score 423;  DB 10; Length 434;
Best Local Similarity   99.8%;  Pred. No. 7.7e-97;
Matches  434;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   1;
```

```
Qy   126  ATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTCATGGGGGGAAGCTGTGGGGCAGA 185
           | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434  ATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTCATGGGGGGAAGCTGTGGGGCAGA 375

Qy   186  TTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCCGAACTGCTCATTTCTGC 245
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374  TTCCTTAAGCGACCCTTT-GGACAACTCTTATCAGGGAGGAGGAGCCGAACTGCTCATTTCTGC 316

Qy   246  CTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAG 305
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315  CTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAG 256

Qy   306  GCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAG 365
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255  GCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAG 196

Qy   366  GTCCTTCATTATTTTGTCCACAGCCAGAGGGCGTCTTTTTGATTTTCCAAAAATCCAGGGAA 425
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195  GTCCTTCATTATTTTGTCCACAGCCAGAGGGCGTCTTTTTGATTTTCCAAAAATCCAGGGAA 136

Qy   426  CTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTCCTTGTTAAGTAGCCTTTATCCCCAGCGAA 485
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135  CTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTCCTTGTTAAGTAGCCTTTATCCCCAGCGAA 76
```

Query Match   34.3%;   Score 411;   DB 4;   Length 441;
Best Local Similarity   100.0%;   Pred. No. 8.5e-94;
Matches   411;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy      1 GGAACTAAAAAAGAACTTAATTATTGAGGGCAAGGGGATGCAAGGGGATGCAAACAATACAAAAAATCAA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 GGAACTAAAAAAGAACTTAATTATTGAGGGCAAGGGGATGCAAGGGGATGCAAACAATACAAAAAATCAA 359

Qy     61 AAGCTTATCGGTATTAACTTTCTTCTTCTGTCAAATGAGAGTTAGATTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 AAGCTTATCGGTATTAACTTTCTTCTTCTGTCAAATGAGAGTTAGATTTTATT 299

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 239

Qy    181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 179

Qy    241 TCTGCCTACTTCTTTCCTTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 TCTGCCTACTTCTTTCCTTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 119

Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 GTGAGGCCCGCAATTAGGGAAAAGAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 59

Qy    361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCC 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCC 8
```

RESULT 26
AAH35326/c
ID   AAH35326 standard; cDNA; 632 BP.
XX
AC   AAH35326;
XX
DT   03-SEP-2001   (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:2408.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US026524.
XX
PR   29-SEP-1999;   99US-0157137P.
PR   03-NOV-1999;   99US-0163280P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG75921.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS   Claim 1; Page 3960; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC   proteins are collectively known as colon cancer antigens. The colon

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RESULT 25
AAF75092/c
ID   AAF75092 standard; cDNA; 441 BP.
XX
AC   AAF75092;
XX
DT   10-MAY-2001   (first entry)
XX
DE   Human colon associated protein cDNA sequence #16.
XX
KW   Human; colon; cancer; disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200112781-A1.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022157.
XX
PR   13-AUG-1999;   99US-0148680P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CE, Rosen CA;
XX
DR   WPI; 2001-147551/15.
XX
PT   Nucleic acids encoding 13 human colon cancer associated polypeptides,
PT   useful for preventing, diagnosing and/or treating e.g. cancers
PT   (especially colon cancer), Parkinson's disease and diabetic retinopathy.
XX
PS   Claim 1; Page 314; 326pp; English.
XX
CC   The present invention relates to 13 human colon cancer-associated
CC   proteins. These proteins and the nucleic acid encoding them may be used
CC   in the prevention, diagnosis and treatment of diseases associated with
CC   inappropriate colon cancer-associated protein expression
XX
SQ   Sequence 441 BP; 158 A; 87 C; 89 G; 107 T; 0 U; 0 Other;

```
Qy    125 CATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGCAG 184
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 CATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGCAG 407

Qy    185 ATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTG 244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 ATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTG 347

Qy    245 CCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATGCATGCAATGGTGA 304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 CCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATGCATGCAATGGTGA 287

Qy    305 GGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCA 364
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286 GGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCA 227

Qy    365 GGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGA 424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 GGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGA 167

Qy    425 ACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGA 484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166 ACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGA 107

Qy    485 ATTTGTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCATTTTGG 544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    106 ATTTGTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCATTTTGG 47

Qy    545 TG 546
          ||
Db     46 TG 45
```

CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 632 BP; 191 A; 139 C; 137 G; 146 T; 0 U; 19 Other;

Query Match   33.0%; Score 396.2; DB 4; Length 632;
Best Local Similarity   95.7%; Pred. No. 5.5e-90;
Matches 424; Conservative   0; Mismatches 16; Indels   3; Gaps   2;

Qy   1 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
              ||||||||||||||||||||||||||||||||||||||| |||| | ||||||||||
Db   512 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGGATGCAACCAATNCAAAAATCAA 453

Qy   61 AAGCTTATCTGGTATTAAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   452 AAGCTTATCTGGTATTAAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 393

Qy   121 TTTACATTTGCT-AAGTGTCCTGAT--CTGCTCATGAAATCCTTCATGGGGGAAGCTGT 177
              |||||||||||| |||||||| || || ||||| ||||| ||||||| || ||||
Db   392 TTTACATTTGCTNAAGTGTCCTGNTTNNGGTCCNTAANTCCTTTNTATGGGNAANCTGT 333

Qy   178 GGGGCAGAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAACTGCTC 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   332 GGGGCAGAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAACTGCTC 273

Qy   238 ATTTCTGCCTACTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATCATTGCATGCA 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   272 ATTTCTGCCTACTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATCATTGCATGCA 213

Qy   298 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACAC 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   212 ATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACAC 153

Qy   358 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   152 TGGTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAAT 93

Qy   418 CCAGGGAACTCCTTTCCATGAG 440
              ||||||||||||||||||||||
Db   92 CCAGGGAACTCCTTTCCATGAG 70

RESULT 27
ADK11672/c
ID   ADK11672 standard; DNA; 350 BP.
XX
AC   ADK11672;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Breast cancer differentially expressed gene product #78.
XX
KW   ds; cytostatic; gene therapy; DKFZp566I133 activity inhibitor;
KW   breast cancer; differential expression.
XX
OS   Homo sapiens.
XX
PN   WO2003057926-A1.
XX
PD   17-JUL-2003.

XX
PF   08-JAN-2003; 2003WO-US000657.
XX
PR   08-JAN-2002; 2002US-035637P.
XX
PA   (CHIR) CHIRON CORP.
XX
PI   Hansen R;
XX
DR   WPI; 2003-577534/54.
XX
PT   Inhibiting a cancerous phenotype of a cell, useful for treating breast
PT   cancer comprises contacting a cancerous mammalian cell with an agent for
PT   inhibition of DKFZp566I133 activity.
XX
PS   Claim 30; SEQ ID NO 78; 257pp; English.
XX
CC   The invention relates to a method of inhibiting a cancerous phenotype of
CC   a cell comprises contacting a cancerous mammalian cell with an agent for
CC   inhibition of DKFZp566I133 activity. The methods are useful for treating
CC   cancer, e.g. breast cancer. This sequence represents a gene product which
CC   is differentially expressed in breast cancer cells. The sequence can be
CC   used in the method of the invention.
XX
SQ   Sequence 350 BP; 96 A; 94 C; 84 G; 76 T; 0 U; 0 Other;

Query Match   29.0%; Score 347.4; DB 10; Length 350;
Best Local Similarity   99.7%; Pred. No. 9.9e-78;
Matches 348; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   273 TACTACAAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGAAAAGAAGCTCTG 332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 TACTACAAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGAAAAGAAGCTCTG 291

Qy   333 GAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAG 392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 GAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAG 231

Qy   393 AGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTCCATGAGTACTCTCAGTC 452
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230 AGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTCCATGAGTACTCTCAGTC 171

Qy   453 CTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGGTTTC 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   170 CTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGGTTTC 111

Qy   513 CATGGCGTGTCCATTGAGATGGCATTGTGTGTGCGAGCGGGGCGAGCGGAGAGGC 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   110 CATGGCGTGTCCATTGAGATGGCATTGTGTGTGCGAGCGGGGCGAGCGGAGAGGC 51

Qy   573 GGGGCGGACGCGTGGGCGGCCTGGGCGAGCTGGGGCGGGGCGGAGAGGC 621
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   50 GGGGCGGACGCGTGGGCGGCCTGGGCGAGCTGGGGCGGGGCGGAGAGGC 2

RESULT 28
ABI99809/c
ID   ABI99809 standard; cDNA; 600 BP.
XX
AC   ABI99809;
XX
DT   07-MAR-2002 (first entry)
XX
DE   Mouse ischaemic condition related cDNA sequence SEQ ID NO:919.
XX
KW   Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW   vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
OS   Mus musculus.
XX
PN   WO200188188-A2.
XX
PD   22-NOV-2001.

```
XX
PF   18-MAY-2001; 2001WO-JP004192.
XX
PR   18-MAY-2000; 2000JP-00145977.
XX
PA   (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI   Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR   WPI; 2002-034733/04.
DR   P-PSDB; ABB57331.
XX
PT   Examining the ischaemic condition (e.g. occlusive ischemia) by measuring
PT   expression levels of particular genes defined in the specification or by
PT   determining the expression profile of a gene group comprising these
PT   genes.
XX
PS   Claim 2; Page 2323-2324; 2690pp; English.
XX
CC   The present invention describes a method for examining ischaemic
CC   conditions, comprising measuring the expression levels of particular
CC   genes (I) in a test sample comprising the expression profile of a
CC   gene group in the sample comprising genes selected from (I). The method
CC   is useful for examining the ischaemic condition (e.g. compressive
CC   ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC   expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC   protein sequences in ABB57020 to ABB57374) or by determining the
CC   expression profile of a gene group comprising these genes. The expression
CC   levels or expression profiles produced by these genes are used as an
CC   indicator when screening for ischaemic condition-improving drugs or
CC   therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC   primers for a mouse ischaemic condition related sequence, which are used
CC   in the exemplification of the present invention
XX
SQ   Sequence 600 BP; 165 A; 140 C; 151 G; 144 T; 0 U; 0 Other;

Query Match             28.7%;  Score 343.6;  DB 6;  Length 600;
Best Local Similarity   79.6%;  Pred. No. 1.1e-76;
Matches  476;  Conservative   0;  Mismatches   99;  Indels  23;  Gaps   5;

Qy      7 AAAAAGAACTTATTATTGAGGGCAAGGGCATGGGATGCAAACATACAAAAATCAAAAGCTT 66
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    591 AAAAAAGGACTTTCTTTATTGAGGGCAATGGGCAATGGGATGCAAACATATAAAACTCAGAAGCTT 532

Qy     67 ATCTGGTAT----TAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
             |||||||     ||| || |||| |||| |||| ||||||| ||| |||||||||
Db    531 CTCTGCCATTGGATTAAGTTTTCTCTCTCAGATTGTTGAGTTGGAGTTGGATCTCATTTG 472

Qy    123 TACATTTGCTAAGTGTCCTGATCGTCTCATGAAATCCTTCATGGGGGAAGCTGTGGGGC 182
          ||||||||||||||||||||||||||||||||                -----GAAGCAGTGGGGC
Db    471 CACATTTCCTAAGGGTCCTGATCGTCCTCACAA---------------GAAGCAGTGGGGC 427

Qy    183 AGATTCCTTAAGCGACCCTTTGG-GACAACTTCTTATCAGGGAGGAGGCGAACTGCTCATTT 241
          ||||||||||||||||||||||| ||||| ||||||||| ||||||||||||| |||||||
Db    426 AGATTCCTCAAGTGACCCCGTGGTGAACACCGCACCAGGGTGGGGTACCAGTGCTCCAGT 367

Qy    242 CTGCCACTACTTCTTCCCTGCTTGCTACTGTGACTACAAAATGCATTGCATGCATGCAATGG 301
          ||||||| || |||||| |||| || ||||| ||||||||||||||||||| |||||||
Db    366 TGGCCTATTCTTCTCCCCTTCTGCTTGCTACTGTTACTACAAAATAGTCATTGCATGCATGCAATGG 307

Qy    302 TGAGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGGT 361
          |||||||| ||||||||||||||||||||||||||| |||||||||||||||||||
Db    306 TGAGCCCGCCACTAGTGATAGAAAGCTCTGGAAGCCCACTTGCCATCTCGGCACTGGT 247

Qy    362 CCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAG 421
          |||||||||| ||||| |||||||||||||||| ||||||||||| ||||||| ||||
Db    246 CCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGATCTTTTGATTTTCCAAAAAACCCAG 187

Qy    422 GGAACTCCTTTCCAGGTACTCCAGGTCCTTATCTCCCCAG 481
          ||||||| ||||| ||||| || || ||||||||||||||
Db    186 GGAACTCCCGTTCCATGAGCACTCCTCAGTCTTTGTCGCCTG 127

Qy    482 CGAATTGTGAAATGTAAACATCATGTTTCCATTGAGATGGCATTT 541
          ||||||||||||||| |||||||||||||||||||||||||||||
Db    126 CAAACCTGTGAAACGTAAGCATCATGTTTCCATGGCGCTGCTGCCATTGGGATGGCCATTT 67
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Qy    542 TGGTGTGTCCGTTGAAGCCTTGG--CCGAGGCGCGGCGACGCTGGGCGAGCTGGGC 597
          |||| ||| ||||||||||||||   |||| ||| |||||||| |||||||| ||||||
Db     66 TGAAG-AGTCTGTCGAAACCTGGGCCCCGAAGCGCAGCAGTCTTGGAAGAGCTGGGC 10
```

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RESULT 29
ADK11671/c
ID   ADK11671 standard; DNA; 341 BP.
XX
AC   ADK11671;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Breast cancer differentially expressed gene product #77.
XX
KW   ds; cytostatic; gene therapy; DKFzp566I133 activity inhibitor;
KW   breast cancer; differential expression.
XX
OS   Homo sapiens.
XX
PN   WO2003057926-A1.
XX
PD   17-JUL-2003.
XX
PF   08-JAN-2003; 2003WO-US000657.
XX
PR   08-JAN-2002; 2002US-0345637P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Hansen R;
XX
DR   WPI; 2003-577534/54.
XX
PT   Inhibiting a cancerous phenotype of a cell, useful for treating breast
PT   cancer comprises contacting a cancerous mammalian cell with an agent for
PT   inhibition of DKFzp566I133 activity.
XX
PS   Claim 30; SEQ ID NO 77; 257pp; English.
XX
CC   The invention relates to a method of inhibiting a cancerous phenotype of
CC   a cell comprises contacting a cancerous mammalian cell with an agent for
CC   inhibition of DKFzp566I133 activity. The methods are useful for treating
CC   cancer, e.g. breast cancer. This sequence represents a gene product which
CC   is differentially expressed in breast cancer cells. The sequence can be
CC   used in the method of the invention.
XX
SQ   Sequence 341 BP; 94 A; 94 C; 80 G; 73 T; 0 U; 0 Other;

Query Match             28.3%;   Score 339.4;  DB 10;  Length 341;
Best Local Similarity   99.7%;   Pred. No. 1e-75;
Matches  340;  Conservative    0;  Mismatches    1;  Indels   0;  Gaps    0;

Qy    281 AATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCA 340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 AATAGTCATTACATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCA 282

Qy    341 CTTTGCCATCTCTACACTGGTCCAGGTCCTTCAGGTACTCCTTG 400
          ||||||||||||||||||||||||||||||||||||||||||||
Db    281 CTTTGCCATCTCTACACTGGTCCAGGTCCTTCAGGTACTCCTTG 222

Qy    401 TTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCCTCCTTTG 460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 TTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCCAGTCCTCCTTTG 162

Qy    461 TTAAGTAGCCTTTATCCCCAGCCTTTATCCCCAGCCTTATCCCCAG 481
          |||||||||||||||||||||||||||||||||||||||||||||
Db    161 TTAAGTAGCCTTTATCCCCAGCCGAATTGTGAAATGTAAACATCATGTTTCCATGGCGT 102

Qy    521 GTTCCATTGAGATGGCATTTTGGTGTGTCCGTTGAAGCCTTGGCCGAGGCGCGGCGGCGA 580
```

Db   101 GTTCCATTTGAGATGGCATTTTGTGTGGTGTGTCCGTTGGACGCGGGCGGCGAGGC 42
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   581 CGCTGGCGGCGAGCTGGGCGAGCTGGACGCGGGGCGGCGAGAGGC 621
            |||||||||||||||||||||||||||||||||||||||||||||
Db   41 CGCTGGGCGAGCTGGGCGAGCTGGACGCGGGGCGGGGCGAGAGGC 1

RESULT 30
AAA46551/c
ID   AAA46551 standard; cDNA; 600 BP.
XX
AC   AAA46551;
XX
DT   25-SEP-2000 (first entry)
XX
DE   cDNA sequence encoding a potassium channel interactor polypeptide.
XX
KW   Potassium channel interactor; PCIP; potassium channel; epilepsy;
KW   spinocerebellar ataxia; nervous system disorder; cardiovascular disorder;
KW   transient outward current; ss.
XX
OS   Rattus sp.
XX
FH   Key   Location/Qualifiers
FT   CDS   52..339
FT   /*tag= a
FT   /product= "potassium channel interactor"
XX
PN   WO200031133-A2.
XX
PD   02-JUN-2000.
XX
PF   19-NOV-1999;   99WO-US027428.
XX
PR   20-NOV-1998;   98US-0109333P.
PR   25-NOV-1998;   98US-0110033P.
PR   30-NOV-1998;   98US-0110277P.
PR   23-APR-1999;   99US-00298731.
PR   09-JUL-1999;   99US-00350614.
PR   09-JUL-1999;   99US-00350874.
PR   21-SEP-1999;   99US-00399913.
PR   21-SEP-1999;   99US-00400492.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (AMHP) AMERICAN HOME PROD CORP.
XX
PI   Rhodes K, Betty M, Ling H, An W;
XX
DR   WPI; 2000-400043/34.
DR   P-PSDB; AAY93492.
XX
PS   Disclosure; Fig 32; 306pp; English.
XX
CC   The present sequence encodes a potassium channel interactor protein
CC   (PCIP). The PCIP polypeptides bind to a potassium channel, modulate the
CC   activity of a potassium channel protein, and/or modulate a potassium
CC   channel mediated activity in a cell. The polynucleotides and polypeptides
CC   are useful in the treatment of epilepsy, and spinocerebellar ataxia, as
CC   well as nervous system related disorders and cardiovascular disorders
CC   associated with abnormal transient outward currents. They are also useful
CC   for identifying compounds which can bind to and modulate the expression
CC   and function of the PCIP nucleic acid molecules and proteins
XX
SQ   Sequence 600 BP; 193 A; 131 C; 137 G; 139 T; 0 U; 0 Other;

Query Match   27.5%; Score 329.8; DB 3; Length 600;
Best Local Similarity   77.8%; Pred. No. 3.6e-73;
Matches 458; Conservative   0; Mismatches 107; Indels   24; Gaps   4;

Qy   7 AAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTT 66
            |||||| |||||||||||||||||||||||||||||||| ||||||||||||||||
Db   569 AAAAAAGACTTTCTTTATTGAGGGCAACCGATGCAAACAATATAAAACTCGAAAGCTC 510

Qy   67 ATCTGGTAT----TTAACTTTCTTCTTCGCTTGTCGTGCTTCAAATGAGAGTTTATTT 122
            |||||||| || |||||||||||| |||||||| ||||| |||||||| |||||
Db   509 CTCTGTCATTGGATTAACTTTCTTCTTCGCTTGTCGTGCTTCGAATTGGAGTTGTATTTG 450

Qy   123 TACATTTGCTAAGTGTCCTGATCTGCTCATGAAAATCCTTCATGGGGAAGCTGTGGGGC 182
            ||||||||||||||||||||||||||||||||||| CAGGAAGCAGTGGGGC 405
Db   449 CACATTTCCTAAGGGTCCTGATCTGCTCA------------

Qy   183 AGATTCCTAAGCGACCCTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTC 242
            ||||||||||||| |||||||||| |||||||||||||||||| | || |||||
Db   404 AGATTCCTCAGTGACCCCATGGGAGAGGAGACCCATCAAGGGTGGGGTACCCAGGC---T 349

Qy   243 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGT 302
            || || || ||| ||||||||||||||||||||||||||||| ||| ||||||||||
Db   348 CCAGTTGGCCTACTTCTTCGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGAT 289

Qy   303 GAGGCCCGCAATAGGAAAAGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
            ||||||| |||||| ||| ||||| |||||||||| | |||||| ||||| ||| ||||
Db   288 GAGCCCGCCACTAGTGATAGAAAGTCTGGAAGCCCACTTTTCCATCTCGGCACTGGTC 229

Qy   363 CAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTGTCTTTTGTTTCAAAATCCAGG 422
            |||||||||||||| |||| ||||||||||||||||||||||| ||| |||||||||
Db   228 CAGGTCTTTCATTATTTTGTCCACAGCCAGAGGGTCCTTTGATTTTGTCCAAAAACCCAGG 169

Qy   423 GAACTCCTTTCCATGAGTACTCCAGTGTTCAATGGCGTGTTCCATTTGAGATGGCATTT 482
            ||||| ||||| ||||| ||||||||||||||| ||||||||||||| | |||||||
Db   168 GAACTCCCTTTCCATGAGCACTCCAGTGTTCAATGGTTTCCATTTGTCAAGTAGTTTTTTCCCCTGC 109

Qy   483 GAATTTGTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCATTT 542
            |||| ||||||||| ||| |||||||| ||| |||| ||| |||||| |||||||||||
Db   108 AAACCTGTGAAATGTAAGCATCATGGTTTCCATGCATCATTTCCATTTGGATGCATTT 49

Qy   543 GGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCGCCGGACGCTCGGCGCGAG 591
            ||||||||||||| |||||||||||||||||||||| ||||||||||||
Db   48 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCCTGCAGTCTTTGGAAG 1

RESULT 31
ABK72684/c
ID   ABK72684 standard; cDNA; 600 BP.
XX
AC   ABK72684;
XX
DT   13-AUG-2002 (first entry)
XX
DE   DNA encoding rat potassium channel interacting protein (PCIP) #13.
XX
KW   Human; rat; mouse; monkey; potassium channel interacting protein; PCIP;
KW   central nervous system disorder; epilepsy; spinocerebellar ataxia; gene;
KW   cardiovascular disorder; amnesia; Alzheimer's disease; memory loss; ss;
KW   affective disorder; sleep disorder; neurodegenerative disorder; stroke;
KW   depression; Parkinson's disease; multiple sclerosis; migraine; angina;
KW   psychiatric disorder; neurological disorder; arteriosclerosis;
KW   restenosis; heart failure; idiopathic cardiomyopathy; gene therapy;
KW   myocardial infarction.
XX
OS   Rattus sp.
XX
PN   WO20022698 4-A2.
XX
PD   04-APR-2002.
XX
PF   27-SEP-2001; 2001WO-US030463.
XX
PR   27-SEP-2000; 2000US-00670756.
PR   31-OCT-2000; 2000US-00703094.
XX
PA   (MILL-) MILLENNIUM PHARM INC.

ID   ABK63467 standard; cDNA; 573 BP.
XX
AC   ABK63467;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Rat sequence differentially expressed in response to a hepatotoxin #1374.
XX
KW   Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
KW   differential expression; centrilobular necrosis; steatosis.
XX
OS   Rattus norvegicus.
XX
PN   WO200210453-A2.
XX
PD   07-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US023872.
XX
PR   31-JUL-2000; 2000US-0222040P.
PR   02-NOV-2000; 2000US-0244880P.
PR   11-MAY-2001; 2001US-0290029P.
PR   15-MAY-2001; 2001US-0290645P.
PR   22-MAY-2001; 2001US-0292336P.
PR   06-JUN-2001; 2001US-0295798P.
PR   13-JUN-2001; 2001US-0297457P.
PR   19-JUN-2001; 2001US-0298884P.
PR   09-JUL-2001; 2001US-0303459P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
XX
DR   WPI; 2002-241625/29.
XX
PT   Predicting toxic effects of compounds or the progression of these toxic
PT   effects by determining the changes in gene expression in tissues or cells
PT   exposed to the toxin and comparing these to gene expression in unexposed
PT   tissues or cells.
XX
PS   Claim 1; SEQ ID NO 1374; 239pp; English.
XX
CC   The invention relates to methods for predicting toxic effects of
CC   compounds or the progression of these toxic effects by determining the
CC   global changes in gene expression in tissues or cells exposed to the
CC   toxin and comparing these to gene expression in unexposed tissues or
CC   cells. Also included are methods of predicting at least one toxic effect
CC   of a compound or progression of a toxic effect, preferably the
CC   hepatotoxicity of a compound, comprising detecting the level of
CC   expression in a tissue or cell sample exposed to the compound of two or
CC   more genes listed in the specification, where differential expression of
CC   the genes is indicative of at least one toxic effect or progression. The
CC   method can also be used to identify an agent which modulates the toxic
CC   response and predict cellular pathways that a compound modulates in a
CC   cell. The methods utilise a set of at least two probes (on a solid
CC   support in kit form), where each of the probes comprises a sequence that
CC   specifically hybridises to a gene listed in the specification, a computer
CC   system comprising a database containing information identifying the
CC   expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC   set of genes comprising at least two genes listed in the specification,
CC   and a user interface to view the information used to present information
CC   identifying the expression level in a tissue or cell of at least one gene
CC   listed in the specification. The method is useful for elucidating global
CC   changes in gene expression and for identifying toxicity markers in
CC   tissues or cell exposed to a known toxin. The genes may be used as
CC   toxicity markers in drug screening and toxicity assays. The genes and
CC   gene expression information may be used as diagnostic markers for the
CC   prediction or identification of the physiological state of tissue or cell
CC   sample that has been exposed to a compound or agent. Hepatotoxicity is
CC   characterised by centrilobular necrosis and steatosis. The present
CC   sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC   which is differentially expressed in response to a hepatotoxic agent
XX

XX
PI   Rhodes K, Betty M, Ling H, An W;
XX
DR   WPI; 2002-416482/44.
DR   P-PSDB; ABG60611.
XX
PT   New isolated potassium channel interactor polypeptide, useful for
PT   treating central nervous system disorder, epilepsy, spinocerebellar
PT   ataxia, cardiovascular disorder, and nervous system related disorders.
XX
PS   Example 21; Fig 32; 259pp; English.
XX
CC   The invention relates to an isolated potassium channel interactor protein
CC   (PCIP) and the polynucleotide encoding it. The DNA and protein sequences
CC   are useful for treating potassium channel associated disorders such as
CC   central nervous system (CNS) disorders, epilepsy, spinocerebellar ataxia,
CC   cardiovascular disorders, amnesia, Alzheimer's related memory loss,
CC   affective disorders, sleep disorders, neurodegenerative disorders such as
CC   Alzheimer's disease, Parkinson's disease and multiple sclerosis,
CC   psychiatric disorders such as depression, neurological disorders such as
CC   migraine and stroke, arteriosclerosis, restenosis, heart failure, angina,
CC   idiopathic cardiomyopathy and myocardial infarction. This sequence
CC   represents cDNA encoding a PCIP of the invention
XX
SQ   Sequence 600 BP; 193 A; 131 C; 137 G; 139 T; 0 U; 0 Other;

Query Match   27.5%; Score 329.8; DB 6; Length 600;
Best Local Similarity   77.8%; Pred. No. 3.6e-73;
Matches   458; Conservative   0; Mismatches 107; Indels 24; Gaps   4;

Qy   7 AAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAACACAATACAAAATCAAAAGCTT 66
            ||||||||||||||||| |||||||||||||||||||||| ||||||| |||| |||||
Db   569 AAAAAAGAACTTTCTTTATTGAGGGCAACCGATGCAACCGATGCAACACAATATAAAACTCGAAAGCTC 510

Qy   67 ATCTGGTAT----TTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
            |||||| |||| | ||||||||||||||||||||||||| ||||||||||
Db   509 CTCTGTCATTGGATTAACTTTTCTTTCTCTGCTTGTCGAATTGGAGTTGGATGTTATTTG 450

Qy   123 TACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGC 182
            |||||||||||||||||||||||||||||||||| ||||||||||
Db   449 CACATTTCCTAAGGGTCCTGATCTGCTCA----------------CAGGAAGCAGTGGGGC 405

Qy   183 AGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGGAGCGAACTGCTCATTC 242
            ||||||||||| |||||||| ||||||| ||||| |||||| ||||||||||||||||||
Db   404 AGATTCCTCAGTGACCCCATGGGAGGAGGACCGCCATCAAGGTGTGGGTACCAGGGC----T 349

Qy   243 TGCCTACTTCTTCCCTTCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGT 302
            |||||||||||||||| |||| ||||||||| |||||||||||||||||||||||
Db   348 CCAGTTGGCCTACTTCTTCTCTGTACTGTACTACAAAATAGTCATTGCATGCAATGAT 289

Qy   303 GAGGCCCGCAATTAGGAGGAAAAGAAAGCCTGAAGCCACCACCTTGCCATCTCTACACTCGGTC 362
            ||||||||| |||||||| || ||| |||||||||||||||||||||||||||||| ||||||
Db   288 GAGCCCCGCCACTAGTGATAGAAAGCTCTGAAGCCACCTTTCCATCTCGGCACTCGGTC 229

Qy   363 CAGGTCCTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG 422
            |||||||||||| |||||||||||||||||||||| ||||||||||||| ||||||||
Db   228 CAGGTCTTCATTATTTTGTCCACAGCCAGAGGGTCCTTTTGATTTTCCAAAAACCCAGG 169

Qy   423 GAACTCCTTTCCATGAGTACTCTCCAGGTCTCCTTGTTAAGTAGCCTTTATCCCCAGC 482
            |||||||||| |||||||||||||||||||||||||||||||||| ||||||||||||
Db   168 GAACTCCCTTTCCATGAGCACTCTCAGTCTCCTTGTTCAAGTAGTTTTTTTCCCCTGC 109

Qy   483 GAATTTGTGAAATGTAAACATCATCATGGTTCCATTGAGTTCCATTGAGATGCATTTT 542
            |||||||||||||||||||||||||||||| ||||||||| |||||||||| ||||||
Db   108 AAACCTGTGAAATGTAAGCATGCATCATGGTTCCATTGGATGCCATTTT 49

Qy   543 GGTGTGGTCCGTTGAAGCCTTGAAGCCTTCCGAGGCGGGCGGGACGCGTGGGCGAG 591
            ||||||| |||| ||||||||| |||||||||||||||||||||||||||||||||
Db   48 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCCTGAGTCTTTGAAG 1

RESULT 32
, ABK63467/c

PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
XX
DR WPI; 2003-689530/65.
XX
PT Predicting a toxic effect of a compound, useful in identifying toxicity
PT markers in liver tissues or cells for drug screening and toxicity assays,
PT comprises preparing gene expression profile of tissue or cells exposed to
PT the compound.
XX
PS Claim 1; SEQ ID NO 3611; 1156pp; English.
XX
CC The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the
CC gene expression profile to a database comprising SEQ ID 1-4925, where
CC differential expression of the gene indicates at least one toxic effect.
CC The method is useful for predicting at least one toxic effect of a
CC compound, predicting hepatotoxicity or the progression of a toxic effect
CC of a compound, identifying an agent that modulates the onset or
CC progression of a toxic response, predicting the cellular pathways that a
CC compound modulates in a cell, and identifying an agent that modulates at
CC least one activity of a protein. The method and compositions of the
CC present invention using a database of genes having liver toxin-induced
CC differential expression, are useful in identifying toxicity markers in
CC liver tissues or cells for drug screening and toxicity assays. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;

Query Match   27.5%;   Score 329.2; DB 10; Length 573;
Best Local Similarity 78.2%;   Pred. No. 4.9e-73;
Matches 455; Conservative 0; Mismatches 103; Indels 24; Gaps 4;

Qy   7 AAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTT 66
         |||||||| |||| ||||||||||||| |||||||||||||| |||| ||||||||||
Db 563 AAAAAAGACTTTCTTTATTGAGGGCAACCGATGCAAACAATATAAAACTCGAAAGCTC 504

Qy   67 ATCTGGTAT---TTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
         ||| |||| |||||||| ||||||||||||||| |||| |||||| |||| ||||||
Db 503 CTCTGTCATTGGATTAACTTTTCTTTCTCTGCTTGTCGAATTGGAGTTGGATGTTATTTG 444

Qy 123 TACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGGC 182
         |||||| |||||| ||||||||||||||| ||||||||||||| |||||||
Db 443 CACATTTCCTAAGGGTCCTGATCTGCTCA---------CAGGAAGCAGTGGGGC 399

Qy 183 AGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGGAACTGCTCATTTC 242
         |||||||| |||| |||||| ||||| ||| |
Db 398 AGATTCCTCAGTTGACCCCATGGGAGAGGACGACCATCAAGGGTGGGTACCAGGGC---T 343

Qy 243 TGCCTACTTCTTTCCCTTCGTGTGCTTCATGTGTACTACAAAATAGTCATTGCATGGT 302
         | ||||||||||| |||||||||||||||||||||||||||||||||||||| ||
Db 342 CCAGTTGGCCTACTTCTTTCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGAT 283

Qy 303 GAGGGCCCGCAATTAGGGAAAAGAAGCTCTCGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
         ||| ||||||| ||| | ||||||||||||| |||||||||| ||||||| |||||||
Db 282 GAGCCCCGCCACTAGTGATAGAAAAGCTCTGGAAGCTCTGGAAGCCCCACTTTTCCATCTCGGCACTGGTC 223

Qy 363 CAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGG 422
         ||||||||||||||||||||||||||| |||||||| ||| ||||||||||||| ||||||
Db 222 CAGGTCTTTCATTATTTTGTCCACAGCGCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 163

Qy 423 GAACTCCTTAAGCGACTACTTCCAGTCTCCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC 482
         ||||||| || ||| | ||||||||||||||||||||||| |||||||| || |||||
Db 162 GAACTCCCTTTCCAGTGAGCACTCTCAGTCCTCCTTTGTCAAGTAGTTTTTTTCCCCTGC 103

Qy 483 GAATTTGTGAAATGTAAACATCATGGTTTCATTGCGTGTTCCATTGGCATTTT 542
         || ||||||||||||| |||||||||||| |||| | ||||||||| ||||
Db 102 AAACCCTGTGAAATGTAAGCATCATGGTTTCCATTGGGATGGCATTTT 43

SQ Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;

Query Match   27.5%;   Score 329.2; DB 6; Length 573;
Best Local Similarity 78.2%;   Pred. No. 4.9e-73;
Matches 455; Conservative 0; Mismatches 103; Indels 24; Gaps 4;

Qy   7 AAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTT 66
Db 563 AAAAAAGACTTTCTTTATTGAGGGCAACCGATGCAAACAATATAAAACTCGAAAGCTC 504

Qy   67 ATCTGGTAT---TTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
Db 503 CTCTGTCATTGGATTAACTTTTCTTTCTCTGCTTGTCGAATTGGAGTTGGATGTTATTTG 444

Qy 123 TACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGGGC 182
Db 443 CACATTTCCTAAGGGTCCTGATCTGCTCA---------CAGGAAGCAGTGGGGC 399

Qy 183 AGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGGAACTGCTGCATTTC 242
Db 398 AGATTCCTCAGTTGACCCCATGGGAGAGGACGACCATCAAGGGTGGGTACCAGGGC---T 343

Qy 243 TGCCTACTTCTTTCCCTTCGTGTGCTTCATGTGTACTACAAAATAGTCATTGCATGGT 302
Db 342 CCAGTTGGCCTACTTCTTTCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGAT 283

Qy 303 GAGGGCCCGCAATTAGGGAAAAGAAGCTCTCGGAAGCCCGCGGGCGACGCT 584
Db 282 GAGCCCCGCCACTAGTGATAGAAAAGCTCTGGAAGCTCTGAGGGCTGCAGTCT 2

Qy 363 CAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGG 422
Db 222 CAGGTCTTTCATTATTTTGTCCACAGCGCAGAGGGTCCTTTGATTTTCCAAAAACCCAGG 163

Qy 423 GAACTCCTTCATGCCATGAGTAACATCATCTCAGTCTCCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC 482
Db 162 GAACTCCCTTTCCATGAGCACTCTCAGTCCTCCTTTGTCAAGTAGTTTTTTTCCCCTGC 103

Qy 483 GAATTTGTGAAATGTAAACATCATGGTTTCATTGCGTGTTCCATTGGCATTTT 542
Db 102 AAACCCTGTGAAATGTAAGCATCATGGTTTCCATTGGGATGGCATTTT 43

RESULT 33
ADB58585/c
ID ADB58585   standard; DNA; 573 BP.
XX
AC ADB58585;
XX
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 3611.
XX
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
KW drug screening; toxicity assay; ds.
XX
OS Unidentified.
XX
PN WO2003064624-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-00060087.
PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.
PR 30-DEC-2002; 2002US-0436643P.
XX

CC   toxicity modelling related gene sequence from the present invention.
XX
SQ   Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;

Query Match   27.5%;   Score 329.2; DB 10;   Length 573;
Best Local Similarity   78.2%;   Pred. No. 4.9e-73;
Matches 455;   Conservative   0; Mismatches 103;   Indels 24;   Gaps   4;

```
Qy        7 AAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACACATACAAAAATCAAAAGCTT 66
            ||||  |  |||||||||||||||||||||||||||||||||||||||  ||| |||||||
Db      563 AAAAAAGACTTTCTTTATTGAGGGCAACCGATGCAAACACATATAAACTCGAAAGCTC 504

Qy       67 ATCTGGTAT---TTAACTTTCTTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATTTT 122
            ||||  ||   ||||||||||||||||||||||||||||||||| ||  ||| ||||||||
Db      503 CTCTGTCATTGGATTAACTTTCTTTCTTCTTCTGCTTGTCGAATTGGAGTTGGATGTTATTTG 444

Qy      123 TACATTTGCTAAGTGTCCTGATCTGCTCATGAAAATCCTTCTATGGGGGGAAGCTGTGGGGC 182
            ||||||||||||||||||||||||||||||||||
Db      443 CACATTTCCTAAGGGTCCTGATCTGCTCA------------------CAGGAAGCAGTGGGGC 399

Qy      183 AGATTCCTTAAGCAGCACACCTTTGGGACAACTCTTATCAGGGAGGAGGGACTGCTCATTTC 242
            ||||||||  | |||||||||||  | |||||||| |||| ||| || ||| ||||||||||
Db      398 AGATTCCTCAGTTGACCCCATGGGAGGAGACGCATCAAGGTGTGGGTACCAGGGC----T 343

Qy      243 TGCCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGGT 302
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      342 CCAGTTGGCCTACTTCTTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGAT 283

Qy      303 GAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
            |||  |||| || | |||||||| || || |||||||||||||||||||||||| ||||
Db      282 GAGCCCCGCCCACTAGTGATAGAAAGCTCTGGAAGCCCACTTTTCCATCTCGGCACTGGTC 223

Qy      363 CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGG 422
            ||||||||| |||| ||||||||||||||||||||||||||||||| |||||||||||
Db      222 CAGGTCTTTCATTATTTTGTCCACAGCCAGAGGGTCCTTTTGATTTTCCAAAAACCCAGG 163

Qy      423 GAACTCCTTTTCCATGAGTACTCTCAGGTCCTTGTTAAGTAGCCTTTATCCCCAGC 482
            |||||||||| |||||||||||||||||||||||||||||| |||||||||| ||
Db      162 GAACTCCCTTTCCATGAGCACTCTCAGGTCCTCTCCTTGTCAAGTAGTTTTTTCCCCTGC 103

Qy      483 GAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTT 542
            |||||||| ||| ||||  ||||||||| ||||||||||||||||||
Db      102 AAACCTGTGAAATGTAAGCATCATGGTTTCCATGGCATGCTCCATTTGGGATGGCATTTT 43

Qy      543 GGTGTGGTCCGTTGAAGCCTTGGCCGAGGCCGCGGCCGGACGCT 584
            | ||| |||| |||||| ||||||||||||||||| |||||||
Db       42 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCAGTCT 2

Qy      543 GGTGTGGTCCGTTGAAGCCTTGGCCGAGGCCGCGGCCGGACGCT 584
            | ||| |||| |||||| ||||||||||||||||| |||||||
Db       42 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCAGTCT 2
```

RESULT 34
ADB53216/c
ID   ADB53216 standard; DNA; 573 BP.
XX
AC   ADB53216;
XX
DT   04-DEC-2003   (first entry)
XX
DE   Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3758.
XX
KW   toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW   toxicity marker; toxicity progression; drug screening;
KW   primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS   Rattus norvegicus.
XX
PN   WO2003065993-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-US003482.
XX
PR   04-FEB-2002; 2002US-0353171P.
PR   13-MAR-2002; 2002US-0363534P.
PR   08-APR-2002; 2002US-0370248P.
PR   10-APR-2002; 2002US-0371134P.
PR   10-APR-2002; 2002US-0371135P.
PR   10-APR-2002; 2002US-0371150P.
PR   11-APR-2002; 2002US-0371413P.
PR   19-APR-2002; 2002US-0373601P.
PR   19-APR-2002; 2002US-0373602P.
PR   22-APR-2002; 2002US-0374139P.
PR   08-MAY-2002; 2002US-0378370P.
PR   09-MAY-2002; 2002US-0378652P.
PR   09-MAY-2002; 2002US-0378653P.
PR   09-MAY-2002; 2002US-0378665P.
PR   09-MAY-2002; 2002US-0394230P.
PR   09-JUL-2002; 2002US-0394253P.
PR   04-SEP-2002; 2002US-0407688P.
PR   28-JAN-2003; 2003US-0442900P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI   Elashoff M;
XX
DR   WPI; 2003-731472/69.
XX
PT   Determining if a compound induces a toxic effect on a tissue or cell, for
PT   identifying hepatotoxic compounds, comprises comparing a gene expression
PT   profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT   mean values.
XX
PS   Claim 44; SEQ ID NO 3758; 874pp; English.
XX
CC   The present invention describes a method for determining whether a
CC   compound induces a toxic effect on a tissue or cell. The method comprises
CC   preparing a gene expression profile of a tissue or cell sample exposed to
CC   the compound, and comparing the gene expression profile to a database
CC   comprising data or information on the Tox mean and non-Tox mean value.
CC   The method is useful for predicting or identifying at least one toxic
CC   effect, particularly hepatotoxicity, of a test or unknown compound. The
CC   genes listed in the specification are useful as diagnostic or toxicity
CC   markers for the prediction or identification of the physiological state
CC   of tissue or cell sample that has been exposed to a compound, or to
CC   identify or predict the toxic effects of a compound or an agent. These
CC   may also be used as markers for monitoring toxicity progression or for
CC   drug screening. The present sequence represents a primary rat hepatocyte

RESULT 35
ABT42181/c
ID   ABT42181 standard; DNA; 573 BP.
XX
AC   ABT42181;
XX
DT   26-JUN-2003   (first entry)
XX
DE   Toxicity modelling related rat gene SEQ ID No 1883
XX
KW   Toxic effect; gene expression profile; renal toxicity; toxicity marker;
KW   database; drug screening; toxicity assay; rat; ds.
XX
OS   Rattus norvegicus.
XX
PN   WO20020295000-A2.
XX
PD   28-NOV-2002.
XX
PF   22-MAY-2002; 2002WO-US016173.
XX
PR   22-MAY-2001; 2001US-0292335P.
PR   13-JUN-2001; 2001US-0297523P.
PR   19-JUN-2001; 2001US-0298925P.

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PR   10-JUL-2001;  2001US-0303807P.
PR   10-JUL-2001;  2001US-0303808P.
PR   10-JUL-2001;  2001US-0303810P.
PR   28-AUG-2001;  2001US-0315047P.
PR   27-SEP-2001;  2001US-0324928P.
PR   22-OCT-2001;  2001US-0330462P.
PR   01-NOV-2001;  2001US-0330867P.
PR   21-NOV-2001;  2001US-0331805P.
PR   06-DEC-2001;  2001US-0336144P.
PR   19-DEC-2001;  2001US-0340873P.
PR   21-FEB-2002;  2002US-0357842P.
PR   21-FEB-2002;  2002US-0357843P.
PR   21-FEB-2002;  2002US-0357844P.
PR   15-MAR-2002;  2002US-0364134P.
PR   08-APR-2002;  2002US-0370144P.
PR   08-APR-2002;  2002US-0370206P.
PR   08-APR-2002;  2002US-0370247P.
PR   17-APR-2002;  2002US-0372794P.
PR   21-APR-2002;  2002US-0371679P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick D,  Porter M,  Johnson K,  Higgs B,  Castle A,  Elashoff M;
XX
DR   WPI; 2003-148464/14.
XX
PT   Predicting at least one toxic effect of a compound, useful for toxicity
PT   modeling, comprises preparing a gene expression profile of a tissue or
PT   cell sample exposed to the compound, and comparing the gene expression
PT   profile to a database.
XX
PS   Example 4; Page; 446pp; English.
XX
CC   The invention relates to a novel method of predicting at least one toxic
CC   effect of a compound. The method comprises a gene expression profile of a
CC   tissue or cell sample exposed to the compound, and comparing the gene
CC   expression profile to a database comprising at least part of the data or
CC   information given in the specification. The methods are useful for
CC   predicting at least one toxic effect of a compound, predicting the
CC   progression of a toxic effect of a compound, predicting the renal
CC   toxicity of a compound, or identifying toxicity markers in tissues or
CC   cells exposed to known renal toxin. The genes are useful as toxicity
CC   markers in drug screening and toxicity assays, in monitoring disease or
CC   physiological states, or disease progression. This polynucleotide
CC   represents a rat DNA sequence relating to the toxic effect database
CC   described in the specification. NOTE: The sequence data for this patent
CC   did not form part of the printed specification, but was obtained in
CC   electronic format directly from the World Intellectual Property
CC   Organization
XX
SQ   Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;

Query Match             27.5%;  Score 329.2;  DB 10;  Length 573;
Best Local Similarity   78.2%;
Matches  455;  Conservative   0;  Mismatches  103;  Indels  24;  Gaps   4;

Qy         7 AAAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAATCAAAAGCTT 66
             ||||| ||||| |||||||||||||||||||||||||||||| |||| |||||||
Db       563 AAAAAAAGACTTCTTATTGAGGGCAACCGATGCAAACAATATAAACTCGAAAGCTC 504

Qy        67 ATCTGTAT---TTAACTTTCTTTCTTTTCTTGCTTGTCAAATGAGAGTTAGATTTTTATTTT 122
             ||||||||   |||||| ||||||||| |||||| ||||||||||||| ||||||
Db       503 CTCTGTCATTGCATTGATTAACTTTTCTTTTCTTTGCTTGTCGAATTGGATTGGATGTTATTTG 444

Qy       123 TACATTTGCTAAGTGCTCCTAGTGTCCTGATCTGCTCATGCATGAGAATCCTTCATGGGGAAGCTGTGGGGC 182
             |||||||| | |||||||||||||||||||||||||||||                |||||||||||||
Db       443 CACATTTCCTAAGGGTCCTAGCTCGATCTGCTCA-----------CAGGAAGCAGTGGGGC 399

Qy       183 AGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGCGGAACTGCTCATTTC 242
             ||||||| || |||  | || ||||||||||||||||||||||||||
Db       398 AGATTCCTCAGTGACCCATGGGGACCCCATGGGGAGGAGGCATCAAGGTGTGGGTACCAGGGC----T 343

Qy       243 TGCCTACTTCTTCCCTTCGTCGTTCGTCATGTGTACTACAAAAAAATAGTCATTGCATGCAATGGT 302
             |||||| | |||||| ||| ||||||| |||||||| ||||||||| |||||| |||||||
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Db       342 CCAGTTGGCCTACTTCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATGAT 283
Qy       303 GAGGCCGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
             ||| |||||||| |||||| |||||| ||||||||||||||| |||
Db       282 GAGCCCGGCCAGTAGTAGAAGAGCTGGAAGCCCACTTTTCCATCTCGGCACTGGTC 223
Qy       363 CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTGATTTTCAAAAATCCAGG 422
             |||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db       222 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCTTTGATTTTCCAAAAACCAGG 163
Qy       423 GAACTCCTTTCCATGAGTACTTCTCAGTCTCTCAGTTGTTAAGTAGCCTTTATCCCCAGC 482
             ||||||||||| |||||||| ||||| ||||||||| ||||||||||||   ||||
Db       162 GAACTCCCTTTCCATGAGCACTCTCAGTCTCCCTTTGTCAGTAGTTTTTTCCCCTGC 103
Qy       483 GAATTTGTGAAATGTAAACATCATGGTTCCATGGCCTGTTCCATTTGAGATGGCATTT 542
             |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       102 AAACCTGGAAAATGTAAGCATCATGGTTTCCATGGCGTCTCCATTTGGGGATGGCATTTT 43
Qy       543 GGTGTGGTCCGTTGAAGCCTTGGCCGAGGGCGGCGGCGGACGGCT 584
             |||||||||||||||||||| |||  |||| ||||||||
Db        42 GAAG-AATCTGTTGAAACCTGGGCCCTGAGCGCCTGCAGTCT 2
```

```
RESULT 36
ABX13102/c
ID   ABX13102 standard; cDNA; 573 BP.
XX
AC   ABX13102;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Rat cDNA encoding small calcium binding protein p11.
XX
KW   Rat; ss; gene; voltage gated sodium channel; VGSC; Nav1.8; p11;
KW   small calcium binding protein; analgesia; chronic pain; osteoarthritis;
KW   rheumatoid arthritis; neuropathic pain; cancer pain;
KW   tri geminal neuralgia; hyperalgesia; inflammatory pain; nociceptive pain;
KW   tabes dorsalis; phantom limb pain; spinal cord injury pain; central pain;
KW   post-herpetic pain; HIV pain; non-cardiac chest pain;
KW   irritable bowel syndrome; bowel disorder.
XX
OS   Rattus norvegicus.
XX
FH   Key            Location/Qualifiers
FT   CDS            46..336
FT                  /*tag= a
FT                  /product= "p11"
XX
PN   WO200301691 7-A2.
XX
PD   27-FEB-2003.
XX
PF   20-AUG-2002; 2002WO-GB003852.
XX
PR   20-AUG-2001; 2001GB-0020238.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Okuse K,  Baker M,  Poon L,  Wood JN,  Malik-Hall M;
XX
DR   WPI; 2003-278589/27.
DR   P-PSDB; ABG76192.
XX
PT   identifying a voltage gated sodium channel (VGSC) modulator for producing
PT   analgesia and for relieving chronic pain, e.g. osteoarthritis or HIV
PT   pain, comprises bringing into contact a VGSC, a p11 peptide and a test
PT   compound.
XX
PS   Disclosure; Page 84-85; 114pp; English.
XX
CC   The invention relates to identifying a modulator of a voltage gated
CC   sodium channel (VGSC) e.g. Nav1.8 comprising: (a) bringing into contact a
```

CC   VGSC, a p11 peptide (a small calcium binding protein of the S-100 family)
CC   and test compound (tc) so that the VGSC and the p11 peptide can form a
CC   complex in the absence of the (tc); and (b) measuring an activity of the
CC   VGSC, where a change in the activity of the VGSC relative to the activity
CC   in the absence of the (tc) indicates that the (tc) is a modulator of
CC   VGSC. Also included are a method of enhancing the functional expression
CC   of a VGSC in a cell by increasing the level of p11 in the cell, a
CC   compound identified by a method above, a host cell capable of expressing
CC   a VGSC and a p11 peptide (where the VGSC and/or peptide 11 is expressed
CC   from one or more heterologous expression vectors within the cell),
CC   treating a disorder or condition associated with the activity of a
CC   voltage gated sodium channel (by administering to an individual a
CC   compound identified by the method above, or an inhibitor of p11 activity
CC   or expression). The method is useful for identifying modulators of VGSC.
CC   Compounds identified as modulator of VGSC are useful for manufacturing a
CC   medicament for modulating the functional expression of a voltage gated
CC   sodium channel, for producing analgesia and for relieving chronic pain
CC   such as osteoarthritis, rheumatoid arthritis, neuropathic pain, cancer
CC   pain, tri geminal neuralgia, primary and secondary hyperalgesia,
CC   inflammatory pain, nociceptive pain, tabes dorsalis, phantom limb pain,
CC   spinal cord injury pain, central pain, post-herpetic pain and HIV pain,
CC   non-cardiac chest pain, irritable bowel syndrome and pain associated with
CC   bowel disorders. The present sequence encodes rat p11
XX
SQ   Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;

Query Match   27.5%; Score 329.2; DB 10; Length 573;
Best Local Similarity   78.2%;   Pred. No. 4.9e-73;
Matches   455; Conservative   0; Mismatches 103; Indels   24; Gaps   4;

Qy   7 AAAAAAGAACTTTATTATTGAGGGCAAGGGGGATGCAAACAATACAAAAATCAAAAGCTT 66
              |||||| |||||||| ||| ||| |||||||||||||| |||||||||||| ||||||||
Db   563 AAAAAAGACTTTCTTATTGAGGGCAACCGGATGCAAACAATAAAAACTCGAAAGCTC 504

Qy   67 ATCTGGTAT---TTAACTTTTCTTTTCTTTTCTTGTTGTCAAATGAGAGTTAGATTTTATTT 122
              |||||||| ||||| || ||| ||||||| ||||| |||||||||||||||||
Db   503 CTCTGTCATTGGATTAACTTTTCTTTTCTTTTCTTGTTGTCAAATGAGAGTTAGATTTTATTTG 444

Qy   123 TACATTTGCTAAGTGTCCTGATCTGCTACGTCTGCTCATGAAATCCTTCTATGGGGGGAGCTGTGGGGC 182
              |||||| ||||||||||||||||| |||||||||||||
Db   443 CACATTTCCTAAGGGTCCTGATCTGCTCA----------CAGGAGCAGTGGGGC 399

Qy   183 AGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTTC 242
              ||||||||| |||||||||||| | | || ||||| ||| |||| || | |||
Db   398 AGATTCCTCAGTTGACCCCATGGGAGGAGGAGGACGCCATCAAGGTGTGGGTACCAGGGC----T 343

Qy   243 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGT 302
              |||||| |||| ||||||||| |||||
Db   342 CCAGTTGGCCCACTTCTTCTGTCTTCTGTCATGTGTACTACAAAATAGTCATTGCATGCAATGAT 283

Qy   303 GAGGCCCGCAATTAGGGAGAGAGAGCTCGGAAGCCCACTTGCCATCTCTACACTGGTC 362
              ||| |||| ||| | || | ||| ||||| ||||| ||||||||||||| ||| |||
Db   282 GAGCCCCGCCACTAGTGATAGAAAGCTCTGGAAGCCCACTTTCCATCTCGGCACTGGTC 223

Qy   363 CAGGTCCTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGG 422
              ||||| ||||||||| ||||||||||| |||||| || ||||| |||||| |||||
Db   222 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCTCTTTGATTTCGATTTTCCAAAAACCCAGG 163

Qy   423 GAACTCCTTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC 482
              ||||||||| |||||| | ||||||||| ||||||| ||| || |||||| |||||||
Db   162 GAACTCCCTTTCCATGAGCACTCCAGGTCCTCCTTTTGTCAAGTAGTTTTTTTTCCCCTGC 103

Qy   483 GAATTTGTGAAATGTAAAACATCATGTTGTTCCATTGTGTGTTCCATTGAGATGGCATTTT 542
              ||||| ||||||||||| | |||||| |||||||||||||||||||||||||||||||||
Db   102 AAACCTGTGAAATGTAAGCAGTCATCATGTTTCCATGGCATGCTCCCATTGGGATGCCGATGGCATTTT 43

Qy   543 GGTGTGGTCCGTTGAAGCCTTGGCCCGAGCCCGGGCCGGACGCT 584
              ||| ||||||| |||||||| | ||| || |||| |||| |||||
Db   42 GAAG-AATCTGTTGAAACCTGGGCCCTGGGCCCTGAGCCGCGTGCAGTCT 2

RESULT 37
, ADP72563/c

ID   ADP72563 standard; DNA; 573 BP.
XX
AC   ADP72563;
XX
DT   26-AUG-2004 (first entry)
XX
DE   Renal toxin progression gene marker #1152.
XX
KW   ds; toxic effect; gene expression profile; kidney tissue;
KW   differential gene expression; toxicity progression; toxicity marker;
KW   drug screening; toxicity assay; kidney pathology; nephritis;
KW   kidney necrosis; glomerular injury; tubular injury;
KW   focal segmental glomerulosclerosis.
XX
OS   Rattus norvegicus.
XX
PN   WO200404598-A2.
XX
PD   10-JUN-2004.
XX
PF   24-NOV-2003; 2003WO-US037556.
XX
PR   22-NOV-2002; 2002US-00301856.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick DL, Porter MW, Johnson KR, Castle A, Higgs B;
PI   Elashoff M;
XX
DR   WPI; 2004-460771/43.
XX
PT   Predicting (the progression of) a toxic effect of a compound, for
PT   monitoring the progression of renal disease states, comprises preparing a
PT   gene expression profile of a kidney tissue or cell sample exposed to the
PT   compound.
XX
PS   Claim 11; SEQ ID NO 1152; 266pp; English.
XX
CC   The invention relates to a method of predicting (the progression of) a
CC   toxic effect of a compound by preparing a gene expression profile of a
CC   kidney tissue or cell sample exposed to the compound and comparing the
CC   gene expression profile to a database, or detecting the level of gene(s)
CC   expression in a tissue or cell sample exposed to the compound, where
CC   differential gene expression compared to a control indicates a toxic
CC   effect (toxicity progression). The method is useful for predicting (the
CC   progression of) at least one toxic effect of a compound. The genes are
CC   useful as toxicity markers in drug screening and toxicity assays. The
CC   methods are useful for predicting the likelihood that a compound or test
CC   agent will induce various specific kidney pathologies, such as nephritis,
CC   kidney necrosis, glomerular and tubular injury, or focal segmental
CC   glomerulosclerosis. The methods are useful for determining the similarity
CC   of a toxic response to one or more individual compounds and for
CC   predicting or elucidating the potential cellular pathways influenced,
CC   induced or modulated by the compound or test agent. The kit is useful for
CC   predicting or modelling the toxic response of a test compound, for
CC   monitoring the progression of renal disease states, for identifying genes
CC   that show promise as new drug targets and for screening known and newly
CC   designed drugs. This sequence corresponds to a gene marker used in the
CC   method of the invention. (Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
XX
SQ   Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;

Query Match   27.5%; Score 329.2; DB 12; Length 573;
Best Local Similarity   78.2%;   Pred. No. 4.9e-73;
Matches   455; Conservative   0; Mismatches 103; Indels   24; Gaps   4;

Qy   7 AAAAAAGAACTTTATTATTGAGGGCAAGGGGGATGCAAACAATACAAAAATCAAAAGCTT 66
              |||||| |||||||| ||| ||| |||||||||||||| |||||||||||| ||||||||
Db   563 AAAAAAGACTTTCTTATTGAGGGCAACCGGATGCAAACAATAAAAACTCGAAAGCTC 504

Qy   67 ATCTGGTAT---TTAACTTTTCTTTTCTTTTCTTGTTGTCAAATGAGAGTTAGATTTTATTT 122

```
Db  503 CTCTGGTCATTGGATTAACTTTCTTTCTTCTGCTTGTCGAATTGAGGTTGGATGTTATTTG  444
                ||||        ||||||||||||||||||  |||   |||||   ||||   ||||||

Qy  123 TACATTTGCTAAGTGTCCTGATCTGCTCATGAAAATCCTTCTATGGGGGAAGCTGTGGGGGC  182
                |||||||  |||| ||||||||||||||||                     |||| |||||
Db  443 CACATTTCCTAAGGGTCCTGATCTGCTCA---------------CAGGAAGCAGTGGGGC  399

Qy  183 AGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTC  242
                |||||||    |||| ||||   |||  ||| |||| || |||||
Db  398 AGATTCCTCAGTTGACCCCATGGGACGCGATCAAGGTGTGGGTACCAGGGC-----T  343

Qy  243 TGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGT  302
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  342 CCAGTTGGCCTACTTCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGAT  283

Qy  303 GAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC  362
                |||  ||||||  ||||| |||||||||||||| ||||||||||| ||||||| |||||||
Db  282 GAGCCCCGCCACTAGTGATAGAAAGCTCTGGAAGAGCCCACTTTTCCATCTCCGGCACTGGTC  223

Qy  363 CAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGG  422
                ||||||| |||||||||||||||||||||||||| |||||||||||  |||||| ||||
Db  222 CAGGTCTTTCATTATTTGTCCACAGCCAGAGGGTCCTTTTGATTTTTCCAAAAACCCAGG  163

Qy  423 GAACTCCTTTCCATGAGTACTCTCCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGC  482
                ||||||| |||||||| |||||||||||||||||||||  |||||    ||   ||| |||
Db  162 GAACTCCCTTTCCATGAGCACTCTCCAGTCCTCCTTTGTCAAGTAGTTTTTTTCCCCTGC  103

Qy  483 GAATTTGTGAAATGTAAAACATCATGGTTTCATGGCGTGTTCCATTTGAGATGGCATTTT  542
                  |  ||||||||||||  ||||||||||| ||||| ||  ||||||| |||||||||||
Db  102 AAACCTGTGAAATGTAAGCATCATGGTTTCCATGGCATGCTCCATTTGGGATGGCATTTT  43

Qy  543 GGTGTGTCCGTTGAAGCCTTGGCCGAGGCCGCCGACGCT  584
                |  | ||||||||||  |||  ||| |||||   |||| |
Db   42 GAAG-AATCTGTTGAAACCTGGGCCCTGAGGCGCTGCAGTCT  2
```

RESULT 38
AAS7410/c
ID   AAS7410 standard; cDNA; 318 BP.
XX
AC   AAS7410;
XX
DT   13-FEB-2002 (first entry)
XX
DE   cDNA #86 encoding portion of a human colon tumour protein.
XX
KW   Human; colon tumour protein; colon cancer; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200173027-A2.
XX
PD   04-OCT-2001.
XX
PF   22-MAR-2001; 2001WO-US009246.
PR   24-MAR-2000; 2000US-0191597P.
PR   04-MAY-2000; 2000US-0202024P.
PR   05-MAY-2000; 2000US-0202189P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Meagher MJ, Xu J, King GE;
XX
DR   WPI; 2001-611627/70.
XX
PT   New colon tumor proteins and related nucleic acid, useful for treatment,
PT   prevention, diagnosis and monitoring of cancer.
XX
PS   Claim 4; Page 75; 299pp; English.
XX
CC   Th present invention relates to the isolation of novel cDNA sequences
CC   encoding for at least an immunogenic portion of human colon tumour

CC   proteins. The sequences of the invention are useful in pharmaceutical
CC   compositions and vaccines for the prevention and treatment of cancers
CC   such as colon cancer. They are also useful for the diagnosis and
CC   monitoring of such cancers. Antibodies to the colon tumour proteins and
CC   antigen presenting cells that express polynucleotides encoding colon
CC   tumour proteins can be used to inhibit the development of cancers. T-
CC   cells that react specifically with colon tumour proteins are useful for
CC   removing tumour cells from samples (e.g. blood) and for cancer treatment.
CC   The polynucleotides sequences are also useful in gene therapy. AAS7325-
CC   AAS8880 represent the cDNA sequences of the invention that encode for
CC   portions of human colon tumour proteins
XX
SQ   Sequence 318 BP; 102 A; 67 C; 67 G; 82 T; 0 U; 0 Other;

Query Match   26.4%; Score 317; DB 4; Length 318;
Best Local Similarity   100.0%; Pred. No. 4.8e-70;
Matches 317; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy   35 GGGGATGCAAACAATACAAAAATCAAAAGCTTATCTGTATTTAACTTTCTTTTCTTCTGC  94
                |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  317 GGGGATGCAAACAATACACAAAAATCAAAAGCTTATCTGTATTTAACTTTCTTTTCTTCTGC  258

Qy   95 TTGTCAAATGAGAGTTAGATTTTATTTTACATTGCTAAGTGTCCTGATCTGCTCATGA  154
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  257 TTGTCAAATGAGAGTTAGATTTTATTTTACATTGCTAAGTGTCCTGATCTGCTCATGA  198

Qy  155 AATCCTTCTATGGGGAAGCTGTGGGGACGATTCCTTAAGCGACCCTTTGGACAACTCT  214
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  197 AATCCTTCTATGGGGAAGCTGTGGGGACGATTCCTTAAGCGACCCTTTGGACAACTCT  138

Qy  215 TATCAGGGAGGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTCTTGCTTCATGTGTA  274
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  137 TATCAGGGAGGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTCTTGCTTCATGTGTA  78

Qy  275 CTACAAAATAGTCATTGCATGCAATGCAATGCTGAGGCCCCGCAATTAGGGAAAAGAAGCTCTGGA  334
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   77 CTACAAAATAGTCATTGCATGCAATGCAATGCTGAGGCCCCGCAATTAGGGAAAAGAAGCTCTGGA  18

Qy  335 AGCCCACTTTGCCATCT  351
                |||||||||||||||||
Db   17 AGCCCACTTTGCCATCT  1
```

RESULT 39
AAC81810/c
ID   AAC81810 standard; cDNA; 294 BP.
XX
AC   AAC81810;
XX
DT   22-FEB-2001 (first entry)
XX
DE   Human S100A10 cDNA.
XX
KW   S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
KW   calcium-binding protein; calcium homeostasis; cardiac muscle;
KW   pumping capacity; myocardial cell; systolic calcium ion release;
KW   sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
KW   valve defect; ss.
XX
OS   Homo sapiens.
XX
PN   DE19915485-A1.
XX
PD   19-OCT-2000.
XX
PF   07-APR-1999;   99DE-01015485.
XX
PR   07-APR-1999;   99DE-01015485.
XX
PA   (KATU/) KATUS H A.
PA   (REMP/) REMPPIS A.
XX
PI   Katus HA, Remppis A;

XX
DR   WPI; 2000-673510/66.
DR   P-PSDB; AAB45540.
XX
PT   Composition containing S100 protein, corresponding nucleic acid or
PT   vector, useful for treating cardiomyopathy and cardiac insufficiency.
XX
PS   Claim 36; Page 17; 36pp; German.
XX
CC   This invention describes a novel composition for treating primary or
CC   secondary cardiomyopathy or cardiac insufficiency contains at least one
CC   S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
CC   fragments, or a gene transfer vector containing (II), optionally
CC   formulated with auxiliaries and/or carriers. (I) are calcium-binding
CC   proteins involved in calcium homeostasis, so their overexpression in
CC   cardiac muscle will improve pumping capacity (and overall capacity) of
CC   the heart. In cultured myocardial cells they increase the contraction and
CC   relaxation rates associated with increased systolic calcium ion release
CC   from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
CC   used to treat cardiomyopathy (CMP) where inherited or caused by
CC   spontaneous mutations and ischemic CMP caused by arteriosclerosis,
CC   dilative CMP caused by toxic/infectious disease, cardiac disease caused
CC   by pulmonary and/or arterial hypertension, and structural disease caused
CC   with reduced contractile force, generally any condition associated
CC   ubiquitously, (I) show tissue-specific expression and treat the
CC   underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
CC   disease
XX
SQ   Sequence 294 BP; 96 A; 57 C; 72 G; 69 T; 0 U; 0 Other;

Query Match   24.5%;   Score 294; DB 3; Length 294;
Best Local Similarity   100.0%;   Pred. No. 3.1e-64;
Matches 294;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   246 CTACTTCTTCCCTTCGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATGGTGAG 305
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   294 CTACTTCTTCCCTTCGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATGGTGAG 235

Qy   306 GCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAG 365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   234 GCCCGCAATTAGGGAAAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAG 175

Qy   366 GTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAATCCAGGGAA 425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   174 GTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAATCCAGGGAA 115

Qy   426 CTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAA 485
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   114 CTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAA 55

Qy   486 TTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT 539
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   54 TTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT 1

RESULT 40
ADA08452
ID   ADA08452 standard; DNA; 291 BP.
XX
AC   ADA08452;
XX
DT   06-NOV-2003 (first entry)
XX
DE   Mammalian annexin II p11 subunit antisense polynucleotide.
XX
KW   Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
KW   plasmin reductase; reduced plasmin protein; anti-angiogenesis activity;
KW   urokinase-type plasminogen activator; A61; annexin II heterotetramer;
KW   annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
KW   protein disulphide isomerase; modulating angiogenesis; mammalian; ss.
XX
OS   Mammalia.

XX
PN   US2003083234-A1.
XX
PD   01-MAY-2003.
XX
PF   26-NOV-2002; 2002US-00304287.
XX
PR   28-NOV-2001; 2001US-0333866P.
XX
PA   (WAIS/) WAISMAN D.
PA   (KWON/) KWON M.
XX
PI   Waisman D, Kwon M;
XX
DR   WPI; 2003-596985/56.
XX
PT   Producing an anti-angiogenesis plasmin fragment, useful for modulating,
PT   e.g. promoting or inhibiting angiogenesis, comprises contacting a
PT   plasminogen polypeptide with a plasminogen activator and a plasmin
PT   reductase.
XX
PS   Claim 33; Page 12; 29pp; English.
XX
CC   The present invention relates to a method for producing an anti-
CC   angiogenesis plasmin fragment. The method comprises contacting a
CC   plasminogen polypeptide with a plasminogen activator and a plasmin
CC   reductase. where a reduced plasmin protein is produced and the anti-
CC   angiogenesis plasmin fragment having anti-angiogenesis activity, is
CC   released from the reduced plasmin protein. The plasminogen activator is
CC   preferably a urokinase-type plasminogen activator. The angiogenesis
CC   plasmin fragment is A61. The plasmin reductase is selected from annexin
CC   II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
CC   disulphide isomerase. The annexin II heterotetramer is associated with a
CC   cell membrane. The method of the invention is useful for modulating (e.g.
CC   promoting or inhibiting) angiogenesis. The present sequence represents
CC   mammalian annexin II p11 subunit antisense polynucleotide.
XX
SQ   Sequence 291 BP; 68 A; 71 C; 57 G; 95 T; 0 U; 0 Other;

Query Match   24.3%;   Score 291; DB 9; Length 291;
Best Local Similarity   100.0%;   Pred. No. 1.8e-63;
Matches 291;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   249 CTTCTTTCCCTTCTGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATGGTGAGCC 308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   CTTCTTTCCCTTCTGCTTCATGTGTACTACACAAAATAGTCATTGCATGCAATGGTGAGCC 60

Qy   309 CGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTC 368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTC 120

Qy   369 CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTC 428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTC 180

Qy   429 CTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 488
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 240

Qy   489 GTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCAT 539
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTTGAGATGGCAT 291

RESULT 41
ADA08453/c
ID   ADA08453 standard; DNA; 291 BP.
XX
AC   ADA08453;
XX
DT   06-NOV-2003 (first entry)
XX
DE   Mammalian annexin II p11 subunit sense polynucleotide.

```
ADP67424
ID   ADP67424 standard; cDNA; 291 BP.
XX
AC   ADP67424;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human p11 antisense polynucleotide SEQ ID NO:5.
XX
KW   p11; p11 activity modulator; plasminogen activation; cytostatic;
KW   antisense therapy; cancer; tumour; tumour growth inhibition; antisense;
KW   gene; ss; human.
XX
OS   Homo sapiens.
XX
PN   WO200454517-A2.
XX
PD   01-JUL-2004.
XX
PF   12-DEC-2003; 2003WO-US040029.
XX
PR   13-DEC-2002; 2002US-0433140P.
XX
PA   (MEDI-) MEDIOMICS LLC.
PA   (WAIS/) WAISMAN D.
XX
PI   Waisman D;
XX
DR   WPI; 2004-487995/46.
XX
PT   Composition useful for inhibiting growth of tumor in patient, modulates
PT   activity of p11 protein and effects change in level of plasminogen
PT   activation by a cell.
XX
PS   Disclosure; SEQ ID NO 5; 140pp; English.
XX
CC   The present invention describes a composition (I) which modulates the
CC   activity of a p11 protein and effects a change in the level of
CC   plasminogen activation by a cell. Also described: (1) making (M1) a
CC   clonal cell line, which involves isolating a cell, then characterising
CC   the activity of a protein produced by the cell or clonal progeny of the
CC   cell, where the protein is involved in plasminogen activation; and (2) a
CC   clonal cell line (II) useful in the identification of composition that
CC   modulate p11 activity, where the clonal cell line is obtained by (M1).
CC   (I) has cytostatic activity, and can be used in antisense therapy. (I) is
CC   useful for modulating the activity of p11 which involves administering
CC   (I) to a cell. The cell can be a human cancer cell, chosen from a HT1080
CC   fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal
CC   adenocarcinoma cell. (I) is also useful for reducing the development of
CC   cancer cell in a patient e.g., mouse which involves administering (I) to a
CC   cancer cell in the patient. (I) is useful for inhibiting the growth of
CC   tumours or inhibiting tumour cell invasion in a patient, which involves
CC   administering (I) to a cancer cell in the patient. (II) is useful for
CC   identifying a composition that modulates p11 activity which involves
CC   administering the composition to (II) obtained by (M1), determining the
CC   change in p11 activity of a cell of the clonal cell line relative to a
CC   cell of a clonal cell line that had not received the composition, and
CC   identifying the composition that produces a change in p11 activity. The
CC   change in p11 activity is a change in the level of plasminogen activation
CC   activity. The present sequence represents a human p11 antisense
CC   polynucleotide sequence (antisense to ADP67425), which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 291 BP; 68 A; 71 C; 57 G; 95 T; 0 U; 0 Other;

Query Match             24.3%;  Score 291;  DB 12;  Length 291;
Best Local Similarity   100.0%;  Pred. No. 1.8e-63;
Matches  291;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    249 CTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCC 308
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCC 60
```

RESULT 42

Vertical side panel (left):

```
XX
KW   Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
KW   plasmin reductase; reduced plasmin protein; anti-angiogenesis activity;
KW   urokinase-type plasminogen activator; A61; annexin II heterotetramer;
KW   annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
KW   protein disulphide isomerase; modulating angiogenesis; mammalian; ss.
XX
OS   Mammalia.
XX
PN   US2003083234-A1.
XX
PD   01-MAY-2003.
XX
PF   26-NOV-2002; 2002US-00304287.
XX
PR   28-NOV-2001; 2001US-0333866P.
XX
PA   (WAIS/) WAISMAN D.
PA   (KWON/) KWON M.
XX
PI   Waisman D,  Kwon M;
XX
DR   WPI; 2003-596985/56.
XX
PT   Producing an anti-angiogenesis plasmin fragment, useful for modulating,
PT   e.g. promoting or inhibiting angiogenesis, comprises contacting a
PT   plasminogen polypeptide with a plasminogen activator and a plasmin
PT   reductase.
XX
PS   Claim 41; Page 12; 29pp; English.
XX
CC   The present invention relates to a method for producing an anti-
CC   angiogenesis plasmin fragment. The method comprises contacting a
CC   plasminogen polypeptide with a plasminogen activator and a plasmin
CC   reductase, where a reduced plasmin protein is produced and the anti-
CC   angiogenesis plasmin fragment having anti-angiogenesis activity, is
CC   released from the reduced plasmin protein. The plasminogen activator is
CC   preferably a urokinase-type plasminogen activator. The angiogenesis
CC   plasmin fragment is A61. The plasmin reductase is selected from annexin
CC   II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
CC   disulphide isomerase. The annexin II heterotetramer is associated with a
CC   cell membrane. The method of the invention is useful for modulating (e.g.
CC   promoting or inhibiting) angiogenesis. The present sequence represents
CC   mammalian annexin II p11 subunit sense polynucleotide.
XX
SQ   Sequence 291 BP; 95 A; 57 C; 71 G; 68 T; 0 U; 0 Other;

Query Match             24.3%;  Score 291;  DB 9;  Length 291;
Best Local Similarity   100.0%;  Pred. No. 1.8e-63;
Matches  291;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    249 CTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCC 308
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    291 CTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAATGGTGAGGCC 232

Qy    309 CGCAATTAGGGAAAAGAGAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTC 368
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    231 CGCAATTAGGGAAAAGAGAGCTCGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTC 172

Qy    369 CTTCATTATTTTGTCCACGCCAGAGGGTCTCTTTTGATTTCCAAAAATCCAGGGACTC 428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 CTTCATTATTTTGTCCACGCCAGAGGGTCTCTTTTGATTTCCAAAAATCCAGGGACTC 112

Qy    429 CTTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 CTTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 52

Qy    489 GTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     51 GTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT 1
```

```
Qy      309  CGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTC  368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  CGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTC  120

Qy      369  CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTC  428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTC  180

Qy      429  CTTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCCGAATTT  488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  CTTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCCGAATTT  240

Qy      489  GTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  GTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT  291
```

RESULT 43
ADP67425/c
ID   ADP67425 standard; cDNA; 291 BP.
XX
AC   ADP67425;
XX
DT   23-SEP-2004 (first entry)
XX
DE   Human pll sense polynucleotide SEQ ID NO:6.
XX
KW   pll; pll activity modulator; plasminogen activation; cytostatic;
KW   antisense therapy; cancer; tumour; tumour growth inhibition; gene; ss;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..291
FT   /*tag= a
FT   /product= "pll"
XX
PN   WO200405451-A2.
XX
PD   01-JUL-2004.
XX
PF   12-DEC-2003; 2003WO-US040029.
XX
PR   13-DEC-2002; 2002US-0433140P.
XX
PA   (MEDI-) MEDIOMICS LLC.
PA   (WAIS/) WAISMAN D.
XX
PI   Waisman D;
XX
DR   WPI; 2004-487995/46.
DR   P-PSDB; ADP67422.
XX
PT   Composition useful for inhibiting growth of tumor in patient, modulates
PT   activity of pll protein and effects change in level of plasminogen
PT   activation by a cell.
XX
PS   Disclosure; SEQ ID NO 6; 140pp; English.
XX
CC   The present invention describes a composition (I) which modulates the
CC   activity of a pll protein and effects a change in the level of
CC   plasminogen activation by a cell. Also described: (1) making (M1) a
CC   clonal cell line, which involves isolating a cell, then characterising
CC   the activity of a protein produced by the cell or clonal progeny of the
CC   cell, where the protein is involved in plasminogen activation; and (2) a
CC   clonal cell line (III) useful in the identification of composition that
CC   modulate pll activity, where the clonal cell line is obtained by (M1).
CC   (I) has cytostatic activity, and can be used in antisense therapy. (I) is
CC   useful for modulating the activity of pll which involves administering
CC   (I) to a cell. The cell can be a human cancer cell, chosen from a HT1080
CC   fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal
CC   adenocarcinoma cell. (I) is also useful for reducing the development of

CC   cancer in a patient e.g., mouse which involves administering (I) to a
CC   cancer cell in the patient. (I) is useful for inhibiting the growth of
CC   tumours or inhibiting tumour cell invasion in a patient, which involves
CC   administering (I) to a cancer cell in the patient. (II) is useful for
CC   identifying a composition that modulates pll activity which involves
CC   administering the composition to (II) obtained by (M1), determining the
CC   change in pll activity of a cell of the clonal cell line relative to a
CC   cell of a clonal cell line that had not received the composition, and
CC   identifying the composition that produces a change in pll activity. The
CC   change in pll activity is a change in the level of plasminogen activation
CC   activity. The present sequence represents a human pll sense
CC   polynucleotide sequence, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 291 BP; 95 A; 57 C; 71 G; 68 T; 0 U; 0 Other;

Query Match   24.3%; Score 291; DB 12; Length 291;
Best Local Similarity   100.0%; Pred. No. 1.8e-63;
Matches 291; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy      249  CTTCTTTCCCTTCTGCTTCATTGTGTACTACAAAAATAGTCATTGCAATGGTGAGGCC  308
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      291  CTTCTTTCCCTTCTGCTTCATTGTGTACTACAAAAATAGTCATTGCAATGGTGAGGCC  232

Qy      309  CGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTC  368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      231  CGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTC  172

Qy      369  CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTC  428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      171  CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTC  112

Qy      429  CTTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCCGAATTT  488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      111  CTTTTCCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCCGAATTT  52

Qy      489  GTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       51  GTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCAT  1
```

RESULT 44
AAI10124
ID   AAI10124 standard; DNA; 464 BP.
XX
AC   AAI10124;
XX
DT   12-OCT-2001 (first entry)
XX
DE   Probe #57 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000670.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0633366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG, Hanzel DK, Chen W, Rank DR;

```
XX
DR    WPI; 2001-488901/53.
XX
PT    Human genome-derived single exon nucleic acid probes useful for analyzing
PT    gene expression in human cervical epithelial cells.
XX
PS    Claim 25; SEQ ID NO 57; 487pp; English.
XX
CC    The present invention relates to human single exon nucleic acid probes
CC    (SENP). The present sequence is one such probe. The SENPs are derived
CC    from human HeLa cells. The SENPs can be used to produce a single exon
CC    microarray, which can be used for measuring human gene expression in a
CC    sample derived from human cervical epithelial cells. By measuring gene
CC    expression, the probes are therefore useful in grading and/or staging of
CC    diseases of the cervix, notably cervical cancer. Note: The sequence data
CC    for this patent did not form part of the printed specification, but was
CC    obtained in electronic format directly from WIPO at
CC    ftp.wipo.int/pub/published_pct_sequences
XX
SQ    Sequence 464 BP; 105 A; 108 C; 101 G; 150 T; 0 U; 0 Other;

Query Match    22.8%;    Score 273.8; DB 4;   Length 464;
Best Local Similarity  78.3%;    Pred. No. 4.9e-59;
Matches  367;  Conservative   0; Mismatches  97;  Indels   5;  Gaps   3;

Qy    46  CAATACAAAAATCAAAAGCTTATCTGGTATTTAACTTTCTTCCTGCTGTCAAATGA 105
              |||||  ||||||||| ||   |||| |||||||||  |||  ||  ||  ||||
Db     1  CAATCCAAAGACCAAAAGCCTATTATTTAATTAAC-TTCCTTTCTTCTTGCTTGTTAGATGA 59

Qy   106  GAGTTAGATTTATTTTTACATTGCTAAGTGTCCTGATCGTCTCATGAAATCCTTCTAT 165
              |||||   |||| |||        ||||||| |||||      ||||| |||
Db    60  GATTTGGATTTGATGTGTCGTTTCTTGGC--CCTGGTCTGCTCATGAAAGCCTTCTAC 117

Qy   166  GGGGGAAGCTGTGGGGCAGAGATTCCTTAAGCGACCCCTTGGGACAACTCCTTATCAGGGAGG 225
              |||||||||||||||||||| ||||| | ||||| |||| |||| | ||||| | ||||| |
Db   118  AGGGGGAAGCTGTGGGGCAGAGGTTCCTATAGCGACTCCTTTGGGAGGAACTCTCACAGGGCTG- 176

Qy   226  AGCGAACTGCTCATTTCTGCCTACTCTTCCCTTCGTTCCCTTCCTTGCTTCATAGGTACTACAAAATAG 285
               ||||||| || | |||||| |  |||| ||||||   || ||||||||| |||||||||||||||||
Db   177  -AGTAATTGCTTAGTTCTGCCTGGTCGTTCCCTTCCCTTCCTTCATAGGTACTACAAAATAG 235

Qy   286  TCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTTG 345
               |  |||  ||| |||||||| ||||| |  | |||| |||| |||||||||   | ||
Db   236  TTGTTGTCCACAGTGGTGAGCCCGCAGTGAGTGAGTGAAAACAAGTTCTGGAAGTTCAGTGTG 295

Qy   346  CCATCTCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGA 405
               | ||| | |||||||||| |||||||||| || ||  |||  ||||||||||||||||
Db   296  CTGTCTTGGCACTGGTCCATGTCCTTCATTGTTCTTCATTGTCTGCGACCCAGAGGGTCTTTTGA 355

Qy   406  TTTTCCAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAG 465
               || ||||||||||| ||||||||||| ||||||||||    |||  |   || || |||
Db   356  TTCTCCAAAATCCAAGGAACTCCTTTCCCATGAGTACTTTTCAGGCGCCCTCCCTTCATTAAG 415

Qy   466  TAGCCTTTATCCCCAGCGAATTGTGAAATGTAAACATCATGGTTTCCA 514
              ||||||| ||||||| || ||| ||||| |||||||  | |||||||
Db   416  TAGCCTTTTATCCCCGGCAAATCTGTGAAACGTAAACACACGGTTTCCA 464
```

```
RESULT 45
ABA51754
ID    ABA51754 standard; DNA; 464 BP.
XX
AC    ABA51754;
XX
DT    01-FEB-2002 (first entry)
XX
DE    Human foetal liver single exon nucleic acid probe #59.
XX
KW    Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS    Homo sapiens.
XX
PN    WO200157277-A2.
```

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XX
PD    09-AUG-2001.
XX
PF    30-JAN-2001; 2001WO-US000669.
XX
PR    04-FEB-2000; 2000US-0180312P.
PR    26-MAY-2000; 2000US-0207456P.
PR    30-JUN-2000; 2000US-0608408.
PR    03-AUG-2000; 2000US-0632366.
PR    21-SEP-2000; 2000US-0234687P.
PR    27-SEP-2000; 2000US-0236359P.
PR    04-OCT-2000; 2000GB-0024263.
XX
PA    (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI    Penn SG, Hanzel DK,   Chen W,   Rank DR;
XX
DR    WPI; 2001-483447/52.
XX
PT    Human genome-derived single exon nucleic acid probes useful for analyzing
PT    gene expression in human fetal liver.
XX
PS    Claim 1; SEQ ID NO 59; 639pp + Sequence Listing; English.
XX
CC    The invention relates to a single exon nucleic acid probe for measuring
CC    human gene expression in a sample derived from human foetal liver. The
CC    single exon nucleic acid probes may be used for predicting, measuring and
CC    displaying gene expression in samples derived from human fetal liver. The
CC    present sequence is a single exon nucleic acid probe of the invention.
CC    Note: The sequence data for this patent did not form part of the printed
CC    specification, but was obtained in electronic format directly from WIPO
CC    at ftp.wipo.int/pub/published_pct_sequences
XX
SQ    Sequence 464 BP; 105 A; 108 C; 101 G; 150 T; 0 U; 0 Other;

Query Match    22.8%;    Score 273.8; DB 4;   Length 464;
Best Local Similarity  78.3%;    Pred. No. 4.9e-59;
Matches  367;  Conservative   0; Mismatches  97;  Indels   5;  Gaps   3;
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Search completed: August 18, 2005, 03:59:11

Thu Aug 18 09:11:21 2005

Job time : 684 secs

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                OM nucleic - nucleic search, using sw model

                    Copyright  GenCore version 5.1.6
                    Copyright (c) 1993 - 2005  Compugen Ltd.

Run on:        August 17, 2005, 23:46:33 ; Search time 3771 Seconds
                                           (without alignments)
                                  12102.641 Million cell updates/sec

Title:         US-10-735-577-16
Perfect score: 1199
Sequence:      1 ggaactaaaaagaacttta.........cgggcttcccgcccccaccgg 1199

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      3239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:  68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
               1: gb_est1:*
               2: gb_est2:*
               3: gb_htc:*
               4: gb_est3:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_gss1:*
               9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	694.8	57.9	753	4	BI827113	BI827113 603077308
c 2	688.2	57.4	769	4	BG437145	BG437145 602488791
c 3	687	57.3	883	6	CD389775	CD389775 AGENCOURT
c 4	668	55.7	679	4	BM785208	BM785208 K-EST0063
c 5	665	55.5	681	5	BU521490	BU521490 AGENCOURT
c 6	663	55.3	671	4	BG774775	BG774775 602662641
c 7	658.8	54.9	912	2	BE729901	BE729901 601564949
c 8	657	54.8	660	3	CR610742	CR610742 full-leng
c 9	657	54.8	660	5	BX362846	BX362846 BX362846
c 10	652.8	54.4	705	6	CD177393	CD177393 AGENCOURT
c 11	652	54.4	670	5	BQ646470	BQ646470 AGENCOURT
c 12	651.6	54.3	737	4	BG339527	BG339527 602437371
c 13	648	54.0	663	4	BM541317	BM541317 AGENCOURT
c 14	646.6	53.9	843	5	BU594774	BU594774 AGENCOURT
c 15	646.4	53.9	669	5	BU183451	BU183451 AGENCOURT
c 16	646.4	53.9	940	5	BQ678300	BQ678300 AGENCOURT
c 17	646.4	53.8	681	4	BG332809	BG332809 602430639
c 18	644	53.7	692	5	BU502376	BU502376 AGENCOURT
c 19	640.6	53.4	807	5	BU602356	BU602356 AGENCOURT
c 20	638	53.2	655	5	BQ073203	BQ073203 AGENCOURT
c 21	636.2	53.1	1125	4	BM549820	BM549820 AGENCOURT
c 22	634.4	52.9	657	5	BI825167	BI825167 603072039
c 23	634	52.9	645	2	BE378444	BE378444 601236785
c 24	632	52.7	655	5	BQ050753	BQ050753 AGENCOURT
c 25	631.4	52.7	856	4	BG335520	BG335520 602403994
c 26	630.8	52.6	666	6	CA431436	CA431436 UI-H-FG1-
c 27	629	52.5	687	4	BM546362	BM546362 AGENCOURT
c 28	628.6	52.4	938	2	BF686811	BF686811 602140775
c 29	628.6	52.4	990	4	BE745512	BE745512 601579889
c 30	628.4	52.4	674	4	BI858258	BI858258 603384021
c 31	628.2	52.4	686	6	CA307888	CA307888 UI-H-FT1-
c 32	627.8	52.4	811	4	BI488419	BI488419 603020917
c 33	627	52.3	665	6	CA412335	CA412335 UI-H-EZO-
c 34	626.4	52.2	641	1	AI749536	AI749536 at30b06.x
c 35	625	52.1	641	5	BQ948995	BQ948995 AGENCOURT
c 36	625	52.1	697	5	BI093074	BI093074 602858171
c 37	622.8	51.9	637	7	CN271600	CN271600 170006000
c 38	621.8	51.9	625	4	BM767559	BM767559 K-EST0050
c 39	621.4	51.8	628	4	BM842132	BM842132 K-EST0119
c 40	621	51.8	794	5	BU860855	BU860855 AGENCOURT
c 41	620	51.7	638	5	BQ943717	BQ943717 AGENCOURT
c 42	620	51.7	898	4	BM461859	BM461859 AGENCOURT
c 43	619.8	51.7	645	4	BG335338	BG335338 602404165
c 44	619.4	51.7	662	5	BU934696	BU934696 AGENCOURT
c 45	619	51.6	619	6	CB158822	CB158822 K-EST0218

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                         ALIGNMENTS

RESULT 1
BI827113/c
LOCUS       BI827113      603077308F1 NIH_MGC_119      753 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603077308F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5169265 5',
            mRNA sequence.
ACCESSION   BI827113
VERSION     BI827113.1  GI:1593863
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 753)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1420 row: p column: 02
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
     source          1..753
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5169265"
                     /tissue_type="medulla"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_119"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.3 kb, insert size range
                     0.9-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 013. Note:
                     this a NIH_MGC Library."
ORIGIN
```

```
COMMENT          Contact: Robert Strausberg, Ph.D.
                 Email: cgapbs-r@mail.nih.gov
                 Tissue Procurement: DCTD/DTP/Gazdar
                 cDNA Library Preparation: Ling Hong/Rubin Laboratory
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Incyte Genomics, Inc.
                 Clone distribution: MGC clone distribution information can be
                 found through the I.M.A.G.E. Consortium/LLNL at:
                 http://image.llnl.gov
                 Plate: LLCM1382 row: f  column: 23
                 High quality sequence stop: 750.
FEATURES         Location/Qualifiers
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                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:4620694"
                 /tissue_type="large cell carcinoma"
                 /lab_host="DH10B (phage-resistant)"
                 /clone_lib="NIH_MGC_18"
                 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
                 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                 into EcoRI/XhoI sites using the following 5' adaptor:
                 GGCACGAG(G). Library constructed by Ling Hong in the
                 laboratory of Gerald M. Rubin (University of California,
                 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                 Superscript II RT (Life Technologies). Note: this is a
                 NIH_MGC Library."

ORIGIN

Query Match         57.4%;    Score 688.2;   DB 4;    Length 769;
Best Local Similarity   97.7%;    Pred. No. 2.1e-157;
Matches  729;  Conservative    0;  Mismatches   14;  Indels   3;  Gaps   3;

Qy    9 AAAAGAACTTATTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTTAT   68
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  746 AAAAAGAACTTATTATTTATTGAGGGCAAGGGATGCAGACCATACCAAAATCAGAGCTTAT  687

Qy   69 CTGGTATTTAACTTTC-TTTCTCCTGCTCGTGTTGTCAAATGAGATTTTAT-TTTTACA  126
          ||||||||||||||| ||| |||||||||||||||||||||||||||||| |||||||
Db  686 CTGGTATTTAACTTTTTCGTTTCTCCTGCTCGTGTTGTCAATGAGATTTTATGTTGTTGAACA  627

Qy  127 TTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAGGAAGCTGTGGGGCAGAT  186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  626 TTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAGGAAGCTGTGGGGCAGAT  567

Qy  187 TCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCC  246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  566 TCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCC  507

Qy  247 TACTTCTTCCCCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGG  306
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  506 TACTTCTTCCCCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGG  447

Qy  307 CCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACACTGGTCCAGG  366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  446 CCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACACTGGTCCAGG  387

Qy  367 TCC-TTCATTATTTTGTCCACAGCCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAA  425
          ||| |||||||| |||||||||||||||||||||||||||||||| |||||||||||||
Db  386 TCCGTTCATTATTTTGTCCACAGCCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAA  327

Qy  426 CTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAA  485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  326 CTCCTGTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAA  267

Qy  486 TTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTTGGT  545
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  266 TTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATTTTGGT  207

Qy  546 GTGGTCCGTTGAAGCCTTGGCCGGAGACGCTGGGCGGCCTGGGCGAGCTGGA  605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  206 GTGGTCCGTTGAAGCCTTGGCCGGAGACGCTGGGCGGCCTGGGCGAGCTGGA  147
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Query Match         57.9%;    Score 694.8;   DB 4;    Length 753;
Best Local Similarity   98.5%;    Pred. No. 5.1e-159;
Matches  743;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    4;

Qy  449 GGTCCTCCTTTGTTGTTAAGTAGCCTTTATCCCCAGCGAATTTGT-GAAATGTAAACATCATG  507
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  753 GGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGCATTGTGGAAATGTACACATCATG  694

Qy  508 GTTT-CCATGGCGTGTTCCATTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCTTGGC  566
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  693 GTTTCCCATGGCGTGTTCCATTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCTTGTC  634

Qy  567 CGAGGGCGGCGGGACGCTGGGCGAGCTGGGCGAGCTGGGCGAGAG-GCGAGC  625
          |||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  633 CGAGGGCTGCGGGACGCTGGGCGAGCTGGGCGAGCTGGGCGAGAGTGCGGAGC  574

Qy  626 GCGGCGGCTGTGCGCCCTTCCTTAGTACGTGCGCGGTGGGTAGAGGGAGGAGGCGGCGGCGG  685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  573 GCGGCGGGCTGTGCGCCCTTCCTTAGTACGTGCGCGGTGGGTAGAGGGAGGAGGCGGGTGCGG  515

Qy  686 GAGCGGGAGGAGCCTGGCGGGCGGCGCGTCCCCAGGGCGCTCCCCCAGCCCTGTCTCCTCCCC  745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  514 GAGCGGGAGGAGCCTGGCGGGCGGCGCGTCCCCAGGGCGCTCCCCCAGCCCTGTCTCCTCCCC  455

Qy  746 TCTTCCTGCCCCCGACTCCCCGACCCCCGGCGCGCGGGCGGCGCGCCACGCCCTGCCCTGCCCC  805
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  454 TCTTCCTGCCCCCGACTCCCCGACCCCCGGCGGCGGGCGGCGCGCCACGCCCTGCCCTGCCCC  395

Qy  806 GGACCCGCCTCGCAGGAGGCCTCGCCCGCCCAGACACAGAGCGTTCTTGTAAACTTCTCTTC  865
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  394 GGACCCGCCTCGCAGGAGGCCTCGCCCGCCCAGACACAGAGCGTTCTTGTAAACTTCTCTTC  335

Qy  866 AGTAGAAACGTGTCTGCTCTCGAATATTTCAGGGCATCCCCACCCTGAGCCTGCCCTTCC  925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  334 AGTAGAAACGGTCCTGCTCTCGAATATTTCAGGGCATCCCCACCCTGAGCCTGCCCTTCC  275

Qy  926 TCTCGGGTTGGTTTGGTTTTAGAAAGTGTACAAAATCAAAGAACCCGCCGTCCTCGCGGGTGGG  985
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  274 TCTCGGGTTTGGTTTTAGAAAGTGTACAAAATCAAAGAACCCGCCGTCCTCGCGGGTGGG  215

Qy  986 CACGCTGGCGCAGAACCAGAGCTAACCGGCTCTGCGCCCACCTACGGGTCTAGGAATTAC  1045
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  214 CACGCTGGCGCAGAACCAGAGCTAACCGGCTCTGCGCCCACCTACGGGTCTAGGAATTAC  155

Qy 1046 TTGCTGGATGACCTGCAGGGAGGTGGCACGTGGAGTCCTATCGACCTCAGAGGCACTATC  1105
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Db  154 TTGCTGGATGACCTGCAGGGAGGTGGCACGTGGAGTCCTATCGACCTCAGAGGCACTATC  95

Qy 1106 AGATTAGCCCTAGGAGGTCCGTCTCGGGGGTCTCGGCCGGCCCGGCCCAGTGGAGGGCGGC  1165
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Db   94 AGATTAGCCCTAGGAGGTCCGTCTCGGGGGTCTCGGCCGGCCCGGCCCAGTGGAGGGCGGC  35

Qy 1166 ACCTCCCCAGAAGCCGGGCTTCCGCCCCACCGG  1199
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Db   34 ACCTCCCCAGAAGCCGGGGCTTCCGCCCCACCGG  1
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```
RESULT 2
BG437145/c
LOCUS       BG437145              769 bp    mRNA    linear    EST 14-MAR-2001
DEFINITION  602488791F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4620694 5',
            mRNA sequence.
ACCESSION   BG437145
VERSION     BG437145.1  GI:13343651
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 769)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
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Qy   181  GCAGATTCCTTAAGGCGACCCCTTTGGGACAACTTCTTATCAGGGAGGAGCGAACTGCTCATT  240
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Db   525  GCAGATTCCTTAAGGCGACCCCTTTGGGACAACTTCTTATCAGGGAGGAGCGAACTGCTCATT  466

Qy   241  TCTGCCTACTTCTTCCCTTCGTTCATGTGTACTACAAAATAGTCATGCAATG  300
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Db   465  TCTGCCTACTTCTTCCCTTCGTTCATGTGTACTACAAAATAGTCATGCAATG  406

Qy   301  GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG  360
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Db   405  GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG  346

Qy   361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  286

Qy   421  GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCCTTGTTAAGTAGCCTTTATCCCCA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCCTTGTTAAGTAGCCTTTATCCCCA  226

Qy   481  GGGAATTTGTGAAATGTAAACATCATGGTTTCCATTGCGTGTTCCATTGAGATGGCATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225  GCAATTTGTGAAATGTAAACATCATGGTTTCCATTGCGTGTTCCATTGAGATGGCATT  166

Qy   541  TTGGTGGTCCGTTGAAGCCTTGGGCCAGGGCGGGGACGCTGGGCGAGCTGGGCGGCGAG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165  TTGGTGGTCCGTTGAAGCCTTGGGCCGGGAGGCGGCGGGCGGGCGGGCGAGCTGGGCGAG  106

Qy   601  CTGGACGCGGGGGCGGAGAGGCGAGGCGCGGGCGTGCGCCTTCCTTAGTACGTGCGCGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105  CTGGACGCGGGGGCGGAGAGGCGAGGCGCGGGCGTGCGCCTTCCTTAGTACGTGCGCGC  46

Qy   661  GGGTGGGTAGAGGGAGGCGGCGGCGGGGA  687
          |||||||||||||||||||||||||||||
Db   45   GGGTGGGTAGAGGGAGGCGGCGGCGGGGA  19
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RESULT 4
BM785208/c
LOCUS       BM785208                679 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0063546 S13KMS5s1 Homo sapiens cDNA clone S13KMS5s1-2-G09 5',
            mRNA sequence.
ACCESSION   BM785208
VERSION     BM785208.1  GI:19133440
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 2  row: G  column: 09
            High quality sequence stop: 679.
FEATURES             Location/Qualifiers
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                     /clone="S13KMS5s1-2-G09"
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Qy   606  CCGCGGGGCGGAGAGGCGGAGGGCGCGGGCCTTCCTTAGTACGTGCGGCGGGGTG  665
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Db   146  CCGCGGGGCGGAGAGGCGGAGGGCGCGGGCCTTCCTTAGTACGTGCGGCGGGGTG  87

Qy   666  GGTAGAGGGAGGCGGCGGGGGGAGGCGGGGAGGCGGGGCTCGGCAGGGCGCTCCC  725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   86   GGTAGAGGGAGGCGGCGGGGGGAGGCGGGGAGGCGGGGCTCGGCAGGGCGCGCTCCC  27

Qy   726  CCAGCCCTGTCTCCTCCCCCCTCTTCC  751
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Db   26   CCAGACCTGTCTCTCCCCCCTCTTCC  1
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RESULT 3
CD389775/c
LOCUS       CD389775                883 bp    mRNA    linear   EST 30-MAY-2003
DEFINITION  AGENCOURT_14305360 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CD389775
VERSION     CD389775.1  GI:31228693
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jamie Thompson, University of WI
            cDNA Library Preparation: Gina Zastrow-Hayes
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDKM72  row: e  column: 19
            High quality sequence start: 8
            High quality sequence stop: 630.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic trophoblasts, made from WA01 stem
                     cells"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_173"
                     /note="Vector: pDONR201; Site 1: attP1; Site 2: attP2;
                     LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
                     LIBR_PROVIDER - Bradfield"
ORIGIN

Query Match             57.3%;  Score 687;  DB 6;  Length 883;
Best Local Similarity   100.0%;  Pred. No. 4.3e-157;
Matches  687;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1    GGAACTAAAAGAAGAACTTATTATTGAGGGCAAGGGGATGCAAACATACAAAAAATCAA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705  GGAACTAAAAGAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAA  646

Qy   61   AAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   645  AAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGTCAAATGAGAGTTAGATTTTATT  586

Qy   121  TTTACATTTGCTAAGTGTCCTGATCTGCTACTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585  TTTACATTTGCTAAGTGTCCTGATCTGCTACTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG  526
```

```
/lab_host="Top10F'"
/clone_lib="S13KMSSs1"
/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tabacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library. After analyzing and sequencing about 2,000 ~
3,000 colonies in original cDNA library, the abundant
cDNAs were selected and amplified by PCR reaction using
vector region primer including T7 promoter as 5' primer
and N(dT)14 as 3' primer. The PCR products were used as
template for synthesis of biotinylated single stranded RNA
by in vitro transcription reaction. The synthesized RNA
probes were hybridized with antisense single stranded
cDNAs prepared from original liberary and incubated with
avidin-gel. After removing DNA-RNA hybrids by centrifuge,
the subtracted cDNA libraries were constructed by
transformaion of the remaining DNA into competent cells E.
coli Top10F' with electroporation method."
```

ORIGIN

```
Query Match      55.7%;   Score 668;  DB 4;  Length 679;
Best Local Similarity   100.0%;   Pred. No. 1.8e-152;
Matches  668;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 GGAACTAAAAAGAACTTATTTATTTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 GGAACTAAAAAGAACTTATTTATTTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  609

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTCGTCGTGCTTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 AAGCTTATCTGGTATTTAACTTTCTTTCTCGTCGTGCTTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  549

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCTATCGGGGAGGAGCGAACTGCTCATT  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 TTTACATTTGCTAAGTGTCCTGATCTGCTTCATGAAATCCTTCTATCGGGGAGGAGCGAACTGCTCATT  489

Qy    181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT  429

Qy    241 TCTGCCACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 TCTGCCACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  369

Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG  309

Qy    361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA  249

Qy    421 GGGAACTCCTTTTCATGAGTACTCTCAGGTTCCTCCTTGTTAAGTAGCCTTTATCCCCA  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 GGGAACTCCTTTTCCATGAGTACTCTCAGGTTCCTCCTTGTTAAGTAGCCTTTATCCCCA  189

Qy    481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGCGTGTCCATTTGGAGATGGCATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGCGTGTTCCATTTGAGATGGCATT  129

Qy    541 TTGGTGTGGTCCGTTGAAGCTTGGCGGAGGCGCGGCGAGCGCGGGAGACGCTGGGCGAG  600
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Db    128 TTGGTGTGGTCCGTTGAAGCTTGGCGGAGGCGCGGCGAGCGCGGGAGACGCTGGGCGAG   69
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    601 CTGGACGCGGGGCGGCGGAGAGGCGGAGAGGCGGCGGCGGCGGTGTGCGCCTTCCTTAGTACGTGCGGC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     68 CTGGACGCGGGGCGGCGGAGAGGCGGAGAGGCGGCGGCGGCGGTGTGCGCCTTCCTTAGTACGTGCGGC    9

Qy    661 GGGTGGGT  668
          ||||||||
Db      8 GGGTGGGT    1
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RESULT 5
BU521490/c

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LOCUS       BU521490   681 bp   mRNA   linear  EST 13-SEP-2002
DEFINITION  AGENCOURT_10152991 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6527353
            5', mRNA sequence.
ACCESSION   BU521490
VERSION     BU521490.1   GI:22829016
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14124 row: c column: 01
            High quality sequence stop: 624.
FEATURES             Location/Qualifiers
     source          1..681
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6527353"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb. "
ORIGIN
```

```
Query Match      55.5%;   Score 665;  DB 5;  Length 681;
Best Local Similarity   99.8%;   Pred. No. 1e-151;
Matches  665;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   0;

Qy      1 GGAACTAAAAAGAACTTATTTATTTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 GGAACTAAAAAGAACTTATTTATTTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  607

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTCGTCGTGCTTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 AAGCTTATCTGGTATTTAACTNTTCTTTCTCGTCGTGCTTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  547

Qy    121 TTTACATTTGCTAAGTGTCCTGATCGTCGCTCATGAAATCCTTCTATCGGGGAAGCTGTGGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 TTTACATTTGCTAAGTGTCCTGATCGTCGCTCATGAAATCCTTCTATCGGGGAAGCTGTGGG  487

Qy    181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  427
```

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ORIGIN

                for average insert size 1.8kb.  Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."

Query Match      55.3%;
Best Local Similarity  99.3%;   Score 663; DB 4;  Length 671;
Matches   666;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;
                                       Pred. No. 3.1e-151;

Qy   250  TTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  309
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   671  TTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  612

Qy   310  GCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGG  369
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   611  GCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGG  552

Qy   370  TTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA  429
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   551  TTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA  492

Qy   430  TTTTCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  489
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   491  TTTTCATGAGTACTCCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  432

Qy   490  TGAAATGTAAACATCATGGTTTCCATTGAGATGGCATTTTGTGTGTG  549
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   431  TGAAATGTAAACATCATGGTTTCCATTGAGATGGCATTTTGTGTGTG  372

Qy   550  TCCGTTGAAGCCTTGGCCTGGGCGAGCGCGGCGGCGACGCGCGGCGGGTA  609
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   371  TCCGTTGAAGCCTTGGCCTGGGCGAGCGCGGCGGCGACGCGCGGCGGGTA  312

Qy   610  GGGCGGAGGAGGCGGCGCGGGAGCGGAGGCGGAGGCTGTGCGCGGCGGCG  669
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311  GGGCGGAGGAGGCGGCGCGGGAGCGGAGGCGGAGGCTGTGCGCGGCGGCG  252

Qy   670  GAGGGAGGCGGCGGCGCGGGAGCGGAGGAGGAGCTCGGCGGGCCTCCCCAG  729
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   251  GAGGGAGGCGGTGCGGGGAGCGGGAGGAGGAGCTCGGCAGGGCGCTCCCCAG  192

Qy   730  CCCTGTCTCCTCCCCCCTTCCTGCCCCCGACTCCCCGACCCCCGGGCCCACG  789
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   191  CCCTGTCTCCTCCCCCCTTCCTGCCCCCGACTCCCCGACCCCCGGGCCCACG  132

Qy   790  CCCTGCCCCTCGCTTCCCGACCCGCTCGCAGAGGCCTCGCCCCCAGAGAGCGTTC  849
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131  CCCTGCCCCTCGCTTCCCGACCCGCTCGCAGAGGCCTCGCCCCCAGAGAGCGTTC  72

Qy   850  TTGTAAACTTCTTCTCAGTAGAAACGTCTCGCTCTCGAATATTTCAGGGCATCCCACC  909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71   TTGTAAACTTCTTCTCAGTAGAAACGGTCCTGCTCTCGAATATTTCAGGGCATCCCACC  12

Qy   910  CTGAGCCTGCC  920
          |||||||||||
Db   11   GTGAGCCTGCC  1

RESULT 7
BE729901/c
LOCUS       BE729901   601564949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3925932 5',
DEFINITION  601564949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3925932 5',
                        912 bp    mRNA     linear   EST 15-SEP-2000
            mRNA sequence.
ACCESSION   BE729901
VERSION     BE729901.1  GI:10143893
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
```

Left column (rotated, second page section):

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Qy   241  TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426  TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  367

Qy   301  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366  GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGG  307

Qy   361  TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306  TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA  247

Qy   421  GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246  GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  187

Qy   481  GCGAATTGTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  GCGAATTGTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT  127

Qy   541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGGGCGGCGGACGCGCGGCGGCGGGCGAG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  TTGGTGTGGTCCGTTGAAGCCTTGGCCGGGCGGCGGACGCGCGGCGGCGGGCGAG  67

Qy   601  CTGGACGCGGGGCGGGAGGAGGCGGAGGCGGCGGGCGGCTGTGCGCCTTCCTTAGTACGTGCGGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66   CTGGACGCGGGGCGGGAGGAGGCGGAGGCGGCGGGCGGCTGTGCGCCTTCCTTAGTACGTGCGGC  7

Qy   661  GGGTGG  666
          ||||||
Db   6    GGGTGG  1

RESULT 6
BG774775/c
LOCUS       BG774775   602662641F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4811026 5',
                        671 bp    mRNA     linear   EST 15-MAY-2001
DEFINITION  602662641F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4811026 5',
            mRNA sequence.
ACCESSION   BG774775
VERSION     BG774775.1  GI:14045092
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 671)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1668 row: a  column: 11
            High quality sequence stop: 666.
FEATURES             Location/Qualifiers
     source          1..671
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4811026"
                     /tissue_type="choriocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_21"
                     /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
```

```
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC/DCTD/DTP
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
           Plate: LLCM753  row: b  column: 13
           High quality sequence stop: 745.
FEATURES           Location/Qualifiers
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                   1..912
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:3925932"
                   /tissue_type="melanotic melanoma"
                   /lab_host="DH10B (phage-resistant)"
                   /clone_lib="NIH MGC_20"
                   /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                   EcoRI; cDNA made by oligo-dT priming. Directionally
                   cloned into EcoRI/XhoI sites using the following 5'
                   adaptor: GGCACGAG(G). Size-selected >500bp for average
                   insert size 1.8kb. Library constructed by Ling Hong in
                   the laboratory of Gerald M. Rubin (University of
                   California, Berkeley) using  ZAP-cDNA synthesis kit
                   (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Query Match             54.9%;  Score 658.8;  DB 2;  Length 912;
Best Local Similarity   97.4%;  Pred. No. 3.4e-150;
Matches  744;  Conservative   0;  Mismatches  12;  Indels   8;  Gaps   7;

Qy   111 AGATTTATTTTACATTTGCTAAGTGTCCTGATCGTCGCTCATGAAATCCTTCTATGGGGG 170
         |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   756 AGATAATTAATTTTACATTTGCTAAGTGTCCTGATCGTCGCTCATG-AATCCTTCTATGGGGA 698

Qy   171 AAGCTGTGGGCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGCGA 230
         | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   697 A--CTGTGGGCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGCGA 640

Qy   231 ACTGCTCATTTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATT 290
         |||||||||||||||||||||||||||||||||||||||||||||||| -AAATAGTCATT
Db   639 ACTGCTCATTTCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTAC-AAATAGTCATT 581

Qy   291 GCATGCAATGTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCCACTTTGCCATC 350
         |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   580 GCATGCAATGTGA-GCCCGCAATTAGGGAAAAGAGCTCTGGAAGCCCCACTTTGCCATC 522

Qy   351 TCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTC 410
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 TCTACACTGGTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTC 462

Qy   411 CAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTCGTTAAGTAGCC 470
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 C-AAAATCCAGGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTCGTTAAGTAGCC 403

Qy   471 TTTATCCCCAGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTG 530
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   402 TTTATCCCCAGCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTG 343

Qy   531 AGATGGCATTTGGTGTGGTCCGTTGAAGCTTGGCCGAGGCGCGGACGCTGGGCGA 590
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   342 AGATGGCATTTGGTGTGGTCCGTTGAAGCTT-GCCGAGGCGCGGACGCTGGGCGA 284

Qy   591 GCTGGGCGAGCTGGACGCGGGGCGGCGGCGGAGAGGGCGGGCGTGTGCCGCCTTCCTTAG 650
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   283 GCTGGGCGAGCTGGACGCGGGGCGGCGGCGGAGAGGGCGGGCGTGTGCCGCCTTCCTTAG 224

Qy   651 TACGTCGCGGCGGGTGGGTAGAGGGAGGAGGCGGCGGCGGAGAGCGGCCGGAGGCGGGCT 710
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   223 TACGTCGCGGCGGGTGGGTAGAGGGAGGAGGCGGCGGCGGAGAGCGGCCGGAGGCGGGCT 164

Qy   711 CGGCAGGGCGCTCCCCCAGCCCTTGTCTCCTCCCCCTTCCTGCCCCCGACTCCCCGAC 770
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   163 CGGCAGGGCGCTCCCCCAGCCCTTGTCTCCTCCCCCTTCCTGCCCCCGACTCCCCGAC 104

Qy   771 CCCGGCGCGCGGGCGCCACGCGCCACCGCCGCCTCCGGACCCGCCGCCTCGCGAGAGGCCTCGCC 830
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   103 CCCGGCGCGCGGGCGCCGCCGCCCTGCCTCGCGCCCC-GACCCGCCGCCTCGGCGAGAGGCCTCGCC 45

Qy   831 CGCCCCAGACAGAGCGTTCTTGTAAACTTCTCTTCAGTAGAAAC 874
         ||||||||||||||||||||||||||||||||||||||||||||
Db   44  CGCCCCAGACAGAGCGTTCTTGTAAACTTCTCTTCAGTAGAAAC 1


RESULT 8
CR610742/c
LOCUS       CR610742         660 bp    mRNA    linear   HTC  21-JUL-2004
DEFINITION  full-length cDNA clone CS0DK004YH20 of HeLa cells Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR610742
VERSION     CR610742.1  GI:50491549
KEYWORDS    HTC; CNSIT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 660)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with NotI and cloned
            into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES           Location/Qualifiers
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                   /db_xref="taxon:9606"
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                   /tissue_type="HeLa cells Cot 25-normalized"
                   /plasmid="pCMVSPORT_6"
ORIGIN

Query Match             54.8%;  Score 657;  DB 3;  Length 660;
Best Local Similarity   100.0%; Pred. No. 9e-150;
Matches  657;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1   GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db   657 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 598

Qy   61  AAGCTTATCTGGTATTGTAACTTTCTTTCTTTCTTTGTCAAATGAGAGTTAGATTTTATT 120
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Db   597 AAGCTTATCTGGTATTGTAACTTTCTTTCTTTCTTTGTCAAATGAGAGTTAGATTTTATT 538

Qy   121 TTTACATTTGTCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   537 TTTACATTTGTCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCGAACTGTGGG 478

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGACGCGAACTGCTCATT 240
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Left column

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Db  477 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCATT 418
Qy  241 TCTGCCTACTTCTTCCCTTCGCTTCTGTACTACAAAATAGTCATTGCATGCAATG 300
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Db  417 TCTGCCTACTTCTTCCCTTCGCTTCTGTACTACAAAATAGTCATTGCATGCAATG 358
Qy  301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACTTTGCCATCTCTACACTGG 360
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Db  357 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACTTTGCCATCTCTACACTGG 298
Qy  361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 420
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Db  297 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 238
Qy  421 GGGAACTCCTTTTGTCCACAGCCAGAGGGTCTTTTTCAAAAATCCA 480
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Db  237 GGGAACTCCTTTTGTCCACAGCCAGAGGGTCTTTTTCAAAAATCCA 178
Qy  481 GCGAATTGTGAAATGTAAACATCATGTTTCCATGGCCGTGTTCCATTGGAGATGGCATT 540
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Db  177 GCGAATTGTGAAATGTAAACATCATGTTTCCATGGCCGTGTTCCATTGGAGATGGCATT 118
Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGGCGGCGACGCGCGGCGGCTGGGCGGCGGAG 600
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Db  117 TTGGTGTGGTCCGTTGAAGCCTTGGCGGCGACGCGCGGCGGCTGGGCGGCGGAG 58
Qy  601 CTGGACGCGGGGGCGGGGAGAGGCGCAGCGGCTGTGCGCCCTTCCTTAGTACGTGC 657
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Db   57 CTGGACGCGGGGGCGGGGAGAGGCGCAGCGGCTGTGCGCCCTTCCTTAGTACGTGC 1
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RESULT 9
BX362846/c
LOCUS       BX362846       660 bp    mRNA    linear    EST  23-APR-2004
DEFINITION  BX362846 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK004YH20 5-PRIME, mRNA sequence.
ACCESSION   BX362846
VERSION     BX362846.2  GI:46552294
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 660)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On May 5, 2003 this sequence version replaced gi:30380679.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            980.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DK004D10QP1&c=980.r.
FEATURES             Location/Qualifiers
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                     /clone="CS0DK004YH20"
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                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
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                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
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Right column

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ORIGIN

Query Match        54.8%;  Score 657;  DB 5;  Length 660;
Best Local Similarity   100.0%;  Pred. No. 9e-150;
Matches   657;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GGAACTAAAAAGAAGAACTTTATTTATTGATTGAGGGCAAGGGATGCAAACAATACAAAATCAA  60
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Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db  597 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 538
Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG 180
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Db  537 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG 478
Qy  181 GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 240
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Db  477 GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT 418
Qy  241 TCTGCCTACTTCTTCCCTTCGCTTCATGTTCATGTTCATGCAATG 300
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Db  417 TCTGCCTACTTCTTCCCTTCGCTTCATGTTCATGTTCATGCAATG 358
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Qy  421 GGGAACTCCTTTTCCATGAGTACTCCAGGTCCTTTTCAAAAATCCCA 480
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Db  177 GCGAATTGTGAAATGTAAACATCATGGTTTCATTGAGATGGCATT 118
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Db  117 TTGGTGTGGTCCGTTGAAGCCTTGGGCCGAGGCGCGGCGACCGTGGGCGGCGGAG 58
Qy  601 CTGGACGCGGGGGCGGGAGAGGCGAGCGAGCGCGCGGGCTGTGCGCCCTTCCTTAGTACGTGC 657
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LOCUS       CD177393       705 bp    mRNA    linear    EST  19-MAY-2003
DEFINITION  AGENCOURT_13977124 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CD177393
VERSION     CD177393.1  GI:30863968
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 705)
AUTHORS     
TITLE       
JOURNAL     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jamie Thompson, University of WI
            cDNA Library Preparation: Gina Zastrow-Hayes
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
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BQ646470/c
LOCUS       BQ646470           670 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8286408 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6299585
            5', mRNA sequence.
ACCESSION   BQ646470
VERSION     BQ646470.1  GI:21770642
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 670)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CGAP (Stanford)
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2512 row: h column: 18
            High quality sequence stop: 640.
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_100"
                     /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Query Match             54.4%;  Score 652;  DB 5;  Length 670;
Best Local Similarity  100.0%;  Pred. No. 1.5e-148;
Matches  652;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATCTGCTCTCATGGTGTGG 180
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Db  532 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATCTGCTCTCATGGTGTGG 473

Qy  181 GCAGATTCCTAAGGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
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Qy  241 TCTGCCTACTCTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTGCATTGCATGCAATG 300
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Qy  301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
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.RESULT 11
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            Plate: NDKM38 row: c column: 22
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                     /tissue_type="embryonic trophoblasts, made from WA01 stem
                     cells"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_173"
                     /note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
                     LIBR PRIMING - oligo dT; METHOD - full-length enriched;
                     LIBR PROVIDER - Bradfield"
ORIGIN

Query Match             54.4%;  Score 652.8;  DB 6;  Length 705;
Best Local Similarity   98.9%;  Pred. No. 9.7e-149;
Matches  657;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    1 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db  624 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 565

Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATCTGCTCTCATGGTGTGG 180
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Db  564 TTTACATTTGCTGAGTGTCCTGATCTCGTCCCATGAAATCCTTCTATCTGCTCTCATGGTGTGG 505

Qy  181 GCAGATTCCTAAGGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
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Db  504 GCAGATTCCTAAGGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 445

Qy  241 TCTGCCTACTCTTCTTCCCTTCGCTTCATGTGTACTACAAAATAGTGCATTGCATGCAATG 300
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Qy  301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
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Db  384 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 325

Qy  361 TCCAGGTCCCTTCATTATTTTGTCCACAGCCAGAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
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Db  324 TCCAGGTCCCTTCATTATTTTGTCCACAGCCAGAGAGGGTCTTTTGATTTTCCAAAAATCCA 265

Qy  421 GGGAACTCCTTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTCCTTTGTTAAGTAGCCTT 480
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Db  264 GGGAACTCCTTCCTTTTCCATGAGTACTCTCCAGGTCCTCCTCCTTTGTTAAGTAGCCTT 205

Qy  481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGCGTGTTCCATTTGAGATGGCATT 540
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Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGGGCGGAGGCGGCGGACGCGTGGGCGAGCTGGGCGAG 600
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Qy  601 CTGGACGCGGGGGCGGAGGCGGCAGCGCGGCGGCCTTCCTTAGTACGTGCGGC 660
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Db  712 AAAAAGAACTTTAGTTAGTTATGAGGGCAAGGGGATGCAAACA--TACAAAATCAAAAGCTCAT  655

Qy   69 CTGGTATTAACTTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTATTTTTTACATT  128
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Qy  129 TGCTAAGTGTCCTGATCTGCTCATGAAAATCCTTCATGGGGAAGCTGTGGGCAGATTC  188
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Db  594 TGCTAAGTGTCCTGATCTGCTCATGAAAATCCTTCATGGGGAA--CTGTGGGCAGATTC  537

Qy  189 CTTAAGGCACCCTTGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATTCTGCCTA  248
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Qy  249 CTTCTTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCC  308
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Qy  309 CGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGGTCCAGGTC  368
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Db  416 CGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGGTCCAGGTC  357

Qy  369 CTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCAGGGAACTC  428
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Qy  429 CTTTTCCATGAGTACTCTCCAGTTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGGAATT  488
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Db  297 CTTTTCCATGAGTACTCTCCAGTTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGGAATT  237

Qy  489 GTGAAATGTAAAACATCATGGTTTCCATTGAGATGGCATTTTGGTGTG  548
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Db  237 GTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATTTTGGTGTG  178

Qy  549 GTCCGTTGAAGCCTTGGCCGAGGCGCGGCGACGCTGGGCGGCTGGACGC  608
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Db  117 GGGGCGGGAGAGGCGAGCGCGGGCCGGCCTTCGCCTTCCTTAGTACGTGCGGGCGGGTGGGT  58

Qy  669 AGAGGGAGGCGGCGGGGAGGGGAGGAGCCCTGCGCGGCGCGCTCCC  725
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Db   57 AGAGGGAGGCGGCGGCGGGGAGGGGAGGAGCCCTGCGCGGCGCGCTCCC  1
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Qy  361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  420
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Db  292 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA  233

Qy  421 GGGAACTCCTTTTCCATGAGTACTCTCCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  480
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Db  232 GGGAACTCCTTTTCCATGAGTACTCTCCAGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  173

Qy  481 GCGAATTTGTGAAATGTAAAACATCATGGTTTCCATTGAGATGGCATT  540
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Db  172 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT  113

Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGCGACGCTGGGCGGCTGGGCGGCGAG  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGGCGACGCTGGGCGGCTGGGCGGCGAG  53

Qy  601 CTGGACGCGGGGCGGGGAGAGGCGAGCGCGCGGGCGCTGTGCGCCCTTCCTTAGTA  652
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   52 CTGGACGCGGGGCGGGGAGAGGCGAGCGCGCGGGCGCTGTGCGCCCTTCCTTAGTA  1
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RESULT 12
BG339527/c
LOCUS   BG339527   737 bp   mRNA   linear   EST 27-FEB-2001
DEFINITION 602437371F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4555216 5',
            mRNA sequence.
ACCESSION   BG339527
VERSION   BG339527.1 GI:13145965
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 737)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LiCM1255 row: n column: 17
            High quality sequence stop: 724.
FEATURES   Location/Qualifiers
     source   1..737
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4555216"
                     /tissue_type="leiomyosarcoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_46"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Query Match   54.3%; Score 651.6; DB 4; Length 737;
Best Local Similarity   96.9%; Pred. No. 1.9e-148;
Matches 695; Conservative   0; Mismatches 17; Indels   5; Gaps   3;

RESULT 13
BM541317/c
LOCUS   BM541317   663 bp   mRNA   linear   EST 20-FEB-2002
DEFINITION AGENCOURT_6493714 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5521398
            5', mRNA sequence.
ACCESSION   BM541317
VERSION   BM541317.1 GI:18769859
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 663)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

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                  http://image.llnl.gov
                  Plate: LLAM12186 row: p column: 07
                  High quality sequence stop: 657.
FEATURES          Location/Qualifiers
     source       1..663
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:521398"
                  /tissue_type="leiomyosarcoma"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_71"
                  /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 2.1 kb.

ORIGIN

Query Match       54.0%;   Score 648;  DB 4;  Length 663;
Best Local Similarity   100.0%;   Pred. No. 1.4e-147;
Matches   648;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy       1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db     648 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 589

Qy      61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     588 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 529

Qy     121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGTGTACTACAAAATAGTCATTGCATGCAATG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     528 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGTGTACTACAAAATAGTCATTGCATGCAATG 469

Qy     181 GCAGATTCCTTAAGGCGACCCTTGGGACAACTCCTTATCAGGGAGGACGGAACTGCTCATT 240
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Db     468 GCAGATTCCTTAAGGCGACCCTTGGGACAACTCCTTATCAGGGAGGACGGAACTGCTCATT 409

Qy     241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     408 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 349

Qy     301 GTGAGGCCCGCAATTAGGGAGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     348 GTGAGGCCCGCAATTAGGGAGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 289

Qy     361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     288 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 229

Qy     421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     228 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA 169

Qy     481 GCGAATTGTGAAATGTAAACATCATGGTTCCATTGCGTGTTCCATTGAGATGCATT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     168 GCGAATTGTGAAATGTAAACATCATGGTTCCATTGCGTGTTCCATTGAGATGCATT 109

Qy     541 TTGGTGGTCCGTTGAAGCCTTGGCCGGAGGCCGGAGGCCGGAGGCCGGAGG 600
           ||||||||||||||||||||||||||||||||||||||||||||||
Db     108 TTGGTGGTCCGTTGAAGCCTTGGCCGGAGGCCGGAGGCCGGAGGCCGGAGG 49

Qy     601 CTGGACGCGGGGCGGGGCGAGAGGCCAGCGGCGCGGCGTGTGCGCCTTCCTT 648
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      48 CTGGACGCGGGGCGGGGCGAGAGGCCAGCGGCGCGGCGTGTGCGCCTTCCTT 1
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RESULT 14
BU594774/c
LOCUS   BU594774   843 bp   mRNA   linear   EST 20-SEP-2002
DEFINITION AGENCOURT_8843010 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6450402
            5', mRNA sequence.
ACCESSION   BU594774
VERSION   BU594774.1 GI:23246533

KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: NCI
            cDNA Library Preparation: Michael Brownstein Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2620 row: p column: 19
            High quality sequence stop: 457.
FEATURES   Location/Qualifiers
     source   1..843
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:6450402"
                  /tissue_type="mixed (pool of 40 RNAs)"
                  /lab_host="DH10B (T1-phage-resistant)"
                  /clone_lib="NIH_MGC_142"
                  /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
                  Site_2: SfiI (ggccgcctcggcc);-Double-stranded cDNA was
                  prepared from a pool of 40 cell line polyA+ RNAs (bladder
                  - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
                  4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
                  kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
                  ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
                  gland - 1.3%, and skin - 2.3%), 5' and 3' adaptors were
                  used in cloning as follows:
                  5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
                  enriched library was constructed using the Clontech
                  Creator SMART kit and size-selected to contain the >0.5 kb
                  size fraction (other fractions present in NIH_MGC_141).
                  Library created in the laboratory of M. Brownstein (NIMH,
                  NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match   53.9%;   Score 646.6; DB 5; Length 843;
Best Local Similarity   99.4%;   Pred. No. 3.3e-147;
Matches   649;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

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Qy       1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db     655 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATCCAAAAATCAA 596

Qy      61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     595 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 536

Qy     121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGTGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     535 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGTGG 476

Qy     181 GCAGATTCCTTAAGGCACCCTTTGGACAACTTCTTATCAGGGAGGAGGAGGCGAACTGCTCATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     475 GCAGATTCCTTAAGGCACCCTTTGGACAACTTCTTATCAGGGAGGAGGAGGCGAACTGCTCATT 416

Qy     241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 356

Qy     301 GTGAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 GTGAGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 300
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Db   355 GTGAGGCCCGCAATTAGGGAAAGAAGAGCTCTGGAAGCCACTTGCCATCTCACACTGG 296
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420

Db   1 GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   648 GGAACTAAAAAGAAACTTTATTTATTGAGGGGCAAGGGGATGCAAACAATACAAAAATCAA 589

Db   61 AAGCTTATCTGGTATTAACTTTCTTCTTCTGTCATGAAATCCTTCGCTTGTCAAATGAGAGTTGAATTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   588 AAGCTTATCTGGTATTAACTTTCTTCTTCTGTCAAATGAGAGTTGAATTTATT 529

Db   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   528 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 469

Db   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGGAGGAGGAACTGCTCATT 240
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Qy   468 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGGAGGAGGAACTGCTCATT 409

Db   241 TCTGCCTACTTCTTCCCTTCGTTCATGTTCATGTACTACAAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   408 TCTGCCTACTTCTTCCCTTCGTTCATGTTCATGTACTACAAAATAGTCATTGCATGCAATG 349

Db   301 GTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCACAGCCAGAGGGTCTTTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   348 GTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCACTTTGCCATCTCTACACTGG 289

Db   361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   288 TCCAAGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 229

Db   421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
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Qy   228 GGGAACTCCTTTTCCATGAGTACTCCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 169

Db   481 GCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCATT 540
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Qy   168 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTTGAGATGGCATT 109

Db   541 TTGGTGTGGTCCGTTGAAGCCTTGGGACCGTGGGACGCTGGGCGGCCGAG 600
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Qy   108 TTGGTGTGTCCGTTGAAGCCTTGGGACCGTGGGACGCGCTGGGCGGCCGAG 49

Db   601 CTGGACGCGGGGCGGGAGAGGCGAGCGGAGCGGGCTGTGCGCCTTCCTT 648
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Qy   48 CTGGACGCGGGGCGGGAGAGGCGAGCGGAGCGGGCTGTGCGCCTTCCTT 1

RESULT 16
BQ678300/c
LOCUS   BQ678300   940 bp   mRNA   linear   EST 15-JUL-2002
DEFINITION   AGENCOURT_8500535 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6294152
             5', mRNA sequence.
ACCESSION   BQ678300
VERSION   BQ678300.1 GI:21790979
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 940)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2498 row: f column: 09
             High quality sequence stop: 579.
FEATURES   Location/Qualifiers

RESULT 15
BU183451/c
LOCUS   BU183451   669 bp   mRNA   linear   EST 04-SEP-2002
DEFINITION   AGENCOURT 7954125 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6110024
             5', mRNA sequence.
ACCESSION   BU183451
VERSION   BU183451.1 GI:22697435
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 669)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2356 row: n column: 09
             High quality sequence stop: 632.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6110024"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

Query Match 53.9%; Score 646.4; DB 5; Length 669;
Best Local Similarity 99.8%; Pred. No. 3.6e-147;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

VERSION   BG332809.1   GI:13139247
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
   ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 681)
   AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
   TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
   JOURNAL   Unpublished (1999)
   COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTO/DTP/Gazdar
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1238 row: m column: 09
           High quality sequence stop: 660.
FEATURES   Location/Qualifiers
   source   1..681
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="IMAGE:4548656"
           /tissue_type="large cell carcinoma"
           /lab_host="DH10B (phage-resistant)"
           /clone_lib="NIH_MGC_18"
           /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
           EcoRI; cDNA made by oligo-dT priming. Directionally cloned
           into EcoRI/XhoI sites using the following 5' adaptor:
           GGCACGAG(G). Library constructed by Ling Hong in the
           laboratory of Gerald M. Rubin (University of California,
           Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
           Superscript II RT (Life Technologies). Note: this is a
           NIH_MGC Library."

ORIGIN

Query Match   53.8%;   Score 645;   DB 4;   Length 681;
Best Local Similarity   99.8%;   Pred. No. 7.8e-147;
Matches   656;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

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Qy      1 GGAACTAAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  60
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Db    656 GGAACTAAAAAAGAAC-TTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 598

Qy     61 AAGCTTATCTGGTATTAACTTTCTTTCTCGCTTGTGTCAAATGAGAGTTAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    597 AAGCTTATCTGGTATTTAACTTTCTTTCTCGCTTGTGTCAAATGAGAGTTAGATTTTATT 538

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    537 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 478

Qy    181 GCAGATTCCTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGACGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477 GCAGATTCCTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGACGAACTGCTCATT 418

Qy    241 TCTGCCTACTTCTTTCCTTCCCTTCCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    417 TCTGCCTACTTCTTTCCTTCCCTTCCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 358

Qy    301 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    357 GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 298

Qy    361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    297 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 238

Qy    421 GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCAGGTCCTGTAAGTAGCCTTATCCCA 480
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Qy    1 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGATGCAAGGGATGCAAACAATACAAAAATCAA 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  656 GTAACTAAAAAGAACTTTATTTATTGAGGGCAAAGGGATGCAAAACAATCCAAAAATCAA 597

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
        |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  596 AAGCTTATCTGGTATTTAACTTTCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 537

Qy  121 TTTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  536 TTTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 477

Qy  181 GCAGATTCCTTAAGCGACACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  476 GCAGATTCCTTAAGCGACACCCTTTGGGACACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 417

Qy  241 TCTGCCTACTTCTTCCCTTCCCTTCCCTTCCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  416 TCTGCCTACTTCTTCCCTTCCCTTCCCTTCCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 357

Qy  301 GTGAGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  356 GTGAGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 297

Qy  361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  296 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCA 237

Qy  421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  236 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 177

Qy  481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 540
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  176 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 117

Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGGCGAG 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  116 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGGCGAG 57

Qy  601 CTGGACGCGGGGCGGGGGCGGAGAGGCGAGGCGCCGGCGTGCGCCCTTCCTTAGTAC 653
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   56 CTGGACGCGGGGCGGGGGCGGAGAGGCGAGGCGCCGGCGTGCGCCCTTCCTTAGTAC 4
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RESULT 19
BU602356/c
LOCUS        BU602356        807 bp        mRNA        linear        EST 20-SEP-2002
DEFINITION   AGENCOURT_10014821 NIH_MGC_142 Homo sapiens cDNA clone
             IMAGE:6496426 5', mRNA sequence.
ACCESSION    BU602356
VERSION      BU602356.1  GI:23254115
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 807)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: NCI
             cDNA Library Preparation: Michael Brownstein Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2675 row: n column: 11
             High quality sequence stop: 569.
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Db  237 GGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 178
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Qy  481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 540

Db  177 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 118
        |||||||||||||||||||||||||||||||||||||||||||||||
Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGGCGAG 600

Db  117 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGGCGAG 58
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  601 CTGGACGCGGGGCGGGGGCGGAGAGGCGAGGCGCCGGCGTGCGCCCTTCCTTAGTACGTGC 657

Db   57 CTGGACGCGGGGCGGGGGCGGAGAGGCGAGGCGCCGGCGTGCGCCCTTCCTTAGTACGTGC 1
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 18
BU502376/c
LOCUS        BU502376        692 bp        mRNA        linear        EST 12-SEP-2002
DEFINITION   AGENCOURT_8905908 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6452219
             5', mRNA sequence.
ACCESSION    BU502376
VERSION      BU502376.1  GI:22806955
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 692)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: NCI
             cDNA Library Preparation: Michael Brownstein Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2625 row: 1 column: 12
             High quality sequence stop: 541.
FEATURES             Location/Qualifiers
     source          1..692
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6452219"
                     /tissue_type="mixed (pool of 40 RNAs)"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_142"
                     /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
                     Site 2: SfiI (ggccgcctcggcc); Double-stranded cDNA was
                     prepared from a pool of 40 cell line polyA+ RNAs (bladder
                     - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
                     4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
                     kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
                     ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
                     gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
                     used in cloning as follows:
                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCCGGG-3' and
                     5'-ATTCTAGAGCCCGACCACATG-dT(30)NN-3'. Full-length
                     enriched library was constructed using the Clontech
                     Creator SMART kit and size-selected to contain the >0.5 kb
                     size fraction (other fractions present in NIH MGC 141).
                     Library created in the laboratory of M. Brownstein (NIMH,
                     NIH). Note: this is a NIH_MGC Library."
ORIGIN
```

Query Match 53.7%; Score 644; DB 5; Length 692;
Best Local Similarity 99.1%; Pred. No. 1.4e-146;
Matches 647; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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FEATURES         Location/Qualifiers
  source         1..807
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:6496426"
                 /tissue_type="mixed (pool of 40 RNAs)"
                 /lab_host="DH10B (T1-phage-resistant)"
                 /clone_lib="NIH_MGC_142"
                 /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
                 Site_2: SfiI (ggccgcctcggcc);Double-stranded cDNA was
                 prepared from a pool of 40 cell line polyA+ RNAs (bladder
                 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
                 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
                 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
                 ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
                 gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
                 used in cloning as follows:
                 5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGG-3' and
                 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
                 enriched library was constructed using the Clontech
                 Creator SMART kit and size-selected to contain the >0.5 kb
                 size fraction (other fractions present in NIH_MGC 141).
                 Library created in the laboratory of M. Brownstein (NIMH,
                 NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match      53.4%;    Score 640.6;  DB 5;  Length 807;
Best Local Similarity  99.2%;  Pred. No. 9.6e-146;
Matches  654;  Conservative    0;  Mismatches   4;  Indels    1;  Gaps    1;

Qy    29 GGCCAAGGGGGATGCAAACAATACAAAAA-TCAAAAGCTTATCTGTATTTAACTTTTCTT   87
         ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   662 GGCCAGGGGGATGCAAACAATACAAAAAATCAAAAGCTTATCTGTATTTAACTTTTCTT  603

Qy    88 TCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTATTTTAT ... GTGCCTGATCTG  147
         ||||||||||||||||||||||||||||||||||||||||
Db   602 TCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTATTTTAT ... GTGCCTGATCTG  543

Qy   148 CTCATGAAATCCTTCATGGGGGGAAGCGTGTGGGGCAGATTCCTTAAGCAGCCCTTTGGGA  207
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542 CTCATGAAATCCTTCATGGGGGGAAGCGTGTGGGGCAGATTCCTTAAGCAGCCCTTTGGGA  483

Qy   208 CAACTTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTGCTTC  267
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482 CAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTCTCGCTTC  423

Qy   268 ATGTGTACTACAAAATAGTCATTGCATGCATGGTGAGGCCCGCAATTAGGGAAAAGAAG  327
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422 ATGTGTACTACAAAATAGTCATTGCATGCATGGTGAGGCCCGCAATTAGGGAAAAGAAG  363

Qy   328 CTCTGGAAGCCCACTTTGCCATCTCCACACTGGTCCAGGTCCTTCATTATTTGTCCACA  387
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   362 CTCTGGAAGCCCACTTTGCCATCTCCACACTGGTCCAGGTCCTTCATTATTTGTCCACA  303

Qy   388 GCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTC  447
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   302 GCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTCCATGAGTACTCTC  243

Qy   448 AGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCAGGCGAATTGTGAAATGTAAACATCATG  507
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 AGGTCCTCCCTTTGTTAAGTAGCCTTTATCCCCAGGCGAATTGTGAAATGTAAACATCATG  183

Qy   508 GTTTCCATGGCGGTCCATTGAGATGGCATTTGGTGTGGTCCGTTGAGCCTTGGCC  567
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 GTTTCCATGGCGGTCCATTGAGATGGCATTTGGTGTGGTCCGTTGAGCCTTGGCC  123

Qy   568 GAGGCGCCGCGGACGCGTGGGCGAGCTGACGCGGGCGGAGGCGCAGCGC  627
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   122 GAGGCGCGGCGGACGCGTGGGCGAGCTGGACGCGGGCGGAGGCGGAGCGC   63

Qy   628 GGCGGGCTGTGCGCGCCTTCCTTAGTACGTGCGGCGGGTGGGTAGAGGGAGGCGCGTGCGGG  686
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Db    62 GGCGGGCTGTGCGCGCCTTCCTTAGTACGTGCGGCGGGTGGGTAGAGGGAGGCGCGTGCGGG    4
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Db

RESULT 20
BQ073203/c
LOCUS          BQ073203                     655 bp    mRNA       linear   EST 02-APR-2002
DEFINITION     AGENCOURT_7051984 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:5805962
               5', mRNA sequence.
ACCESSION      BQ073203
VERSION        BQ073203.1  GI:11992249
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 655)
  AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
  TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL      Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: ATCC
               cDNA Library Preparation: Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM2046 row: a  column: 03
               High quality sequence stop: 624.

FEATURES       Location/Qualifiers
  source       1..655
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:5805962"
               /tissue_type="epidermoid carcinoma, cell line"
               /lab_host="DH10B (phage-resistant)"
               /clone_lib="NIH_MGC_101"
               /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
               XhoI; cDNA made by oligo-dT priming. Directionally cloned
               into EcoRI/XhoI sites using the following 5' adaptor:
               GGCACGAG(G). Library constructed by Ling Hong in the
               laboratory of Gerald M. Rubin (University of California,
               Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
               Superscript II RT (Life Technologies). Note: this is a
               NIH_MGC Library."

ORIGIN

Query Match      53.2%;    Score 638;  DB 5;  Length 655;
Best Local Similarity  100.0%;  Pred. No. 4e-145;
Matches  638;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 GGAACTAAAAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   638 GGAACTAAAAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  579

Qy    61 AAGCTTATCTGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   578 AAGCTTATCTGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT  519

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGAAATCCTTCATGTGGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   518 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGAAATCCTTCATGTGGG  459

Qy   181 GCAGATTCCTTAAGCAGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   458 GCAGATTCCTTAAGCAGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT  399

Qy   241 TCTGCCTACTTCTTTCCCTTCTGCTTCCTTCTGCTTCCTTCTGCTACTACAAAATAGTCATTGCATGCAATG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   398 TCTGCCTACTTCTTTCCCTTCTGCTTCCTTCTGCTTCCTTCTGCTACTACACAAAATAGTCATTGCATGCAATG  339
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Qy   301  GTGAGGGCCCGCAATTAGGGAAAAGAAGCTCTGAAGCCACTTGCCATCTCTACACTGG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   338  GTGAGGGCCCGCAATTAGGGAAAAGAAGCTCTGAAGCCACTTGCCATCTCTACACTGG  279

Qy   361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCCA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   278  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCCA  219

Qy   421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   218  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCA  159

Qy   481  GCGAATTTGTGAAATGTAAACATCATGTTTCCATTGAGATGGCATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   158  GCGAATTTGTGAAATGTAAACATCATGTTTCCATTGAGATGGCATT  99

Qy   541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCGGCGGGACCGTGGGCGAGCTGGGCGAG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    98  TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCGGCGGGACCGTGGGCGAGCTGGGCGAG  39

Qy   601  CTGGACCGGCGGGGGCGGGAGAGGCGGAGCGGAGCGGCGGGGCTGTG  638
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    38  CTGGACCGGCGGGGGCGGGAGAGGCGGAGCGGAGCGGCGGGGCTGTG  1
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RESULT 21
BM549820/c
LOCUS   BM549820   1125 bp   mRNA   linear   EST 20-FEB-2002
DEFINITION AGENCOURT_6544034 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5745830
            5', mRNA sequence.
ACCESSION   BM549820
VERSION   BM549820.1 GI:18785543
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1125)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12769 row: g column: 15
            High quality sequence stop: 613.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5745830"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated adult donors. Library is oligo-dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

Query Match   53.1%; Score 636.2; DB 4; Length 1125;

Best Local Similarity   99.5%; Pred. No. 1.2e-144;
Matches 638; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy     1  GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  60
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Db   656  GGAACTAAAAAGAAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA  597

Qy    61  AAGCTTATCTGGTATTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   596  AAGCTTATCTGGTATTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT  537

Qy   121  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   536  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG  477

Qy   181  GCAGATTCCTTAAGCGACAACCCTTTGGGACAACCTTATCAGGAGGAGGAGCGAACTGCTCATT  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   476  GCAGATTCCTTAAGCGACAACCCTTTGGGACAACCTTATCAGGAGGAGGAGCGAACTGCTCATT  417

Qy   241  TCTGCCTACTCTTCTTCCCTTCATGTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   416  TCTGCCTACTCTTCTTCCCTTCATGTGCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG  357

Qy   301  GTGAGGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGG  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   356  GTGAGGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCACTTGCCATCTCTACACTGG  297

Qy   361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCCA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   296  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCCA  237

Qy   421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   236  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCA  177

Qy   481  GCGAATTTGTGAAATGTAAACATCATGTTTCCATTGAGATGGCATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   176  GCGAATTTGTGAAATGTAAACATCATGTTTCCATTGAGATGGCATT  117

Qy   541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCGGCGGGACCGTGGGCGAGCTGGGCGAG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   116  TTGGTGTGGTCCGTTGAAGCCTTGGCCGGAGGCGGCGGGACCGTGGGCGAGCTGGGCGAG  57

Qy   601  CTGGACCGGCGGGGGCGGGAGAGGCGGAGCGGAGCGGCGGGGCTGTGCGC  641
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    56  CTGGACCGGCGGGGGCGGGAGAGGCGGAGCGGAGCGGCGGGGCTGATCCC  16
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RESULT 22
BI825167/c
LOCUS   BI825167   657 bp   mRNA   linear   EST 04-OCT-2001
DEFINITION 603072039F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164209 5',
            mRNA sequence.
ACCESSION   BI825167
VERSION   BI825167.1 GI:15936717
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 657)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov

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LOCUS           BE378444              645 bp    mRNA      linear    EST 21-JUL-2000
DEFINITION      601236785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608925 5',
                mRNA sequence.
ACCESSION       BE378444
VERSION         BE378444.1  GI:9323909
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 645)
AUTHORS         NIH-MGC http://mgc.nci.nih.gov/.
TITLE           National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL         Unpublished (1999)
COMMENT         Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: ATCC
                cDNA Library Preparation: Ling Hong/Rubin Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLCM262 row: i  column: 22
                High quality sequence stop: 639.
FEATURES             Location/Qualifiers
     source          1..645
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3608925"
                     /tissue_type="endometrium, adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_44"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Query Match       52.9%;  Score 634;  DB 2;  Length 645;
Best Local Similarity   99.8%;  Pred. No. 3.8e-144;
Matches 645;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy    255 TCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAAT 314
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    645 TCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGTGA-GCCCGCAAT 587

Qy    315 TAGGGAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTCCACTGTCCTTCAT 374
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 TAGGGAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTCCACTGTCCTTCAT 527

Qy    375 TATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTC 434
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 TATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTC 467

Qy    435 CATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCACGCGAATTGTGAAA 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 CATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCACGCGAATTGTGAAA 407

Qy    495 TGTAAACATCATGGTTTCCATTGGCGTGTTCCATTGAGATGGCATTTTGGTGTGGTCCGT 554
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 TGTAAACATCATGGTTTCCATTGGCGTGTTCCATTGAGATGGCATTTTGGTGTGGTCCGT 347

Qy    555 TGAAGCCTTGGCCGAGGCGCGACGCTGGGCGAGCTGGGCGAGCTGGACGCGGGGGCG 614
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 TGAAGCCTTGGCCGAGGCGCGACGCTGGGCGAGCTGGGCGAGCTGGACCCGGGGGCG 287

Qy    615 GAGAGGCAGCCGCCGCCGCGGCGTGCGCCTCCTTAGTACGTGCGGCGGTGGGTAGAGGG 674
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Plate: LLAM1407 row: m  column: 10
High quality sequence stop: 651.
FEATURES             Location/Qualifiers
     source          1..657
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5164209"
                     /tissue_type="medulla"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_119"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.3 kb, insert size range
                     0.9-3 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 013. Note:
                     this is a NIH_MGC Library."
ORIGIN

Query Match       52.9%;  Score 634.4;  DB 4;  Length 657;
Best Local Similarity   99.8%;  Pred. No. 3.1e-144;
Matches 635;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGAACTAAAAAGAAGAACTTATTATTGAGGGCAAGGGGATGCAAGGGGATCCAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 GGAACTAAAAAGAAGAACTTATTATTGAGGGCAAGGGGATGCAAGGGGATCCAAAATCAA 577

Qy     61 AAGCTTATCTGTATTTAACTTTCTTCTTCCGCTTGTCAAATGAGAGTTAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 AAGCTTATCTGTATTTAACTTTCTTCTTCCGCTTGTCAAATGAGAGTTAGATTTTATT 517

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 457

Qy    181 GCAGATTCCTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456 GCAGATTCCTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCTGCTCATT 397

Qy    241 TCTGCCACTTCTTTCCCTTCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 TCTGCCTACTTCTTTCCCTTCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 337

Qy    301 GTGAGGCCCGCAATTAGGGAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336 GTGAGGCCCGCAATTAGGGAAAGAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 277

Qy    361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 217

Qy    421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCA 157

Qy    481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTGAGATGGCATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 GCGAATTGTGAAATGTAAACATCATGGTTTCCATTGGCGTGTTCCATTGAGATGGCATT 97

Qy    541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGACGCTGGGCGAGCTGGGCGAGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGCGACGCTGGGCGAGCTGGGCGAGCTG 37

Qy    601 CTGGACGCGGGGGCGGAGAGGCGGAGAGGCAGCCGCCGCGGCGGGGGCTG 636
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db     36 CTGGACGCGGGGGCGGAGAGGCGGAGAGGCAGCCGCCGCGGCGGGGGCTG 1

RESULT 23
, BE378444/c
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Db  286 GAGAGGCGCGAGCGCGCGGCGGCTGTGCGCCTTCCTTAGTACGTGCGGCGGTGGGTAGAGGG 227
        |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  675 AGGCGGCGGGGAGCGGGAGGGAGGCCTGGGGCGGCCTCCGCAGGCCCTG 734
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  226 AGGCGGCGGGGAGCGGGAGGGAGGCCTGGGGCGGCGGCCTCCGCAGGCCCTG 167

Qy  735 TCTCCTCCCCTCTTCCTGCCCCCCGACTCCCCCGACCCCCGGCGGCGGCCCACGCCCTG 794
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  166 TCTCCTCCCCTCTTCCTGCCCCCCGACTCCCCCGACCCCCGGCGCGGCCCACGCCCTG 107

Qy  795 CCCTCGCTCCCGACCGCCGCCTCGCAGAGGCCTCGCCGCCCCCAGACAGAGAGCGTTCTTGTA 854
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  106 CCCTCGCTCCCGACCGCCGCCTCGCAGAGGCCTCGCCGCCCCCAGACAGAGAGCGTTCTTGTA 47

Qy  855 AACTTCTCTTCAGTAGAAACGGTCCTGCTCTCGAATATTTCAGGGC 900
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db   46 AACTTCTCTTCAGTAGAAACGGTCCTGCTCTCGAATATTTCAGGGC 1
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RESULT 24

BQ050753/c

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LOCUS       BQ050753            655 bp    mRNA       linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6808933 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784763
            5', mRNA sequence.
ACCESSION   BQ050753
VERSION     BQ050753.1  GI:19810093
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 655)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12870 row: m column: 20
            High quality sequence stop: 654.
FEATURES             Location/Qualifiers
     source          1..655
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5784763"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.1 kb. "
ORIGIN
```

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Query Match         52.7%;  Score 632;  DB 5;  Length 655;
Best Local Similarity  100.0%;  Pred. No. 1.2e-143;
Matches  632;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  632 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 573

Qy   61 AAGCTTATCTGGTATTTAAACTTTTTCTTTCTTTCTGTTCTGCTTGTCAAATGAGAGTTAGAGATTTTATT 120
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  572 AAGCTTATCTGTATTTAAACTTTTTCTTTTCTTTCTGTTCTGCTTGTCAAATGAGAGTTAGAGATTTTATT 513

Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGTGGG 180
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Db  512 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 453
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Qy  181 GCAGATTCCTTAAGCGACACCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
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Db  452 GCAGATTCCTTAAGCGACACCTTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 393

Qy  241 TCTGCCTACTCTTCTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  392 TCTGCCTACTCTTCTTCCCTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 333

Qy  301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACCTTTGCCATCTCTACACTGG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  332 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGAAGCCCACCTTTGCCATCTCTACACTGG 273

Qy  361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  272 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 213

Qy  421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCTTTATCCCCA 480
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Db  212 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCTTTATCCCCA 153

Qy  481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 540
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Db  152 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGAGATGGCATT 93

Qy  541 TTGGTGTGTCCGTTGAAGCCTTGGCCGAGGGCGCCGAGCGCTGGGCGGAG 600
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Db   92 TTGGTGTGTCCGTTGAAGCCTTGGCCGAGGGCGCCGAGCGCTGGGCGGAG 33

Qy  601 CTGACGCGGGGCGGAGAGGCGAGCGCGGCGG 632
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db   32 CTGACGCGGGGCGGAGAGGCGAGCGCGGCGG 1
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RESULT 25

BG335520/c

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LOCUS       BG335520            856 bp    mRNA       linear   EST 27-FEB-2001
DEFINITION  602403994F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541711 5',
            mRNA sequence.
ACCESSION   BG335520
VERSION     BG335520.1  GI:13141958
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1220 row: k  column: 24
            High quality sequence start: 4
            High quality sequence stop: 666.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4541711"
                     /tissue_type="choriocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_21"
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RESULT 26
CA431436
LOCUS       CA431436                  666 bp    mRNA     linear    EST 07-NOV-2002
DEFINITION  UI-H-FGI-bgp-m-06-0-UI.s1 NCI_CGAP_FGI Homo sapiens cDNA clone
            UI-H-FGI-bgp-m-06-0-UI 3', mRNA sequence.
ACCESSION   CA431436
VERSION     CA431436.1  GI:24794162
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..666
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FGI-bgp-m-06-0-UI"
                     /tissue_type="Cell lines"
                     /dev_stage="Adult"
                     /lab_host="DH10B (life Technologies)"
                     /clone_lib="NCI_CGAP_FGI"
                     /note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     NCI CGAP FGI is a normalized cDNA library obtained from a
                     pool of mRNA from 2 cell lines from Enchondroma tissues.
                     The library was constructed according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is CGGTCACTC. The cell lines were provided by Dr.
                     James Martin from the University of Iowa.
                     TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
                     TAG_LIB=UI-H-FGI
                     TAG_SEQ=CGGTCACTC"
ORIGIN
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Query Match   52.6%;   Score 630.8;   DB 6;   Length 666;
Best Local Similarity   99.5%;   Pred. No. 2.3e-143;
Matches 643; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy     1 GGAACTAAAAAAGAACTTTATTTATTG-AGGGCAAGGGGATGCAAACAATACAAAAATCA   59
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    19 GGAACTAAAAAAGAACTTTATTTATTGNAGGGCAAGGGGATGCAAACAATACAAAAATCA   78

Qy    60 AAAGCTTATCTGTATTTAACTTTCTTTCTTGCTTGTCAAATGAGAGTTAGATTTTAT    119
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    79 AAAGCTTATCTGTATTTAACTTTCTTTCTTGCTTGTCAAATGAGAGTTAGATTTTAT    138

Qy   120 TTTTACATTTGCTAAGTGTCCTGATCGTGCTCATGAAATCCTTCTATGGGGAAGCTGTGG   179
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   139  TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTCTGG  198
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   180  GGCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT  239
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199  GGCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT  258
Qy   240  TTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT  299
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259  TTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT  318
Qy   300  GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG  359
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319  GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG  378
Qy   360  GTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCC  419
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379  GTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCC  438
Qy   420  AGGGAACTCCTTTTCCATGAGTACTCTCCAGTCCTCCTTGTTAAGTAGTAGCCTTTATCCCC  479
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439  AGGGAACTCCTTTTCCATGAGTACTCTCCAGTCCTCCTTGTTAAGTAGCCTTTATCCCC  498
Qy   480  AGCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCAT  539
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   499  AGCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCAT  558
Qy   540  TTTGGTGGTCCGTTGAAGCCTTGGCCGAGGGCGCGGACGGCGGGCGAGCTGGGCGA  599
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   559  TTTGGTGGTCCGTTGAAGCCTTGGCCGAGGGCGCGGACGGCGGGCGAGCTGGGCGA  618
Qy   600  GCTGGACGCGGGGCGGGGCGGAGGCCGAGCCGCGGCGGGGCTGTGCGCCTTC  645
                |||||||||||||| |||||||||||||||||||||||||
Db   619  GCTGGACGCGGGGCGGGGCGGAGGCCGAGCCGCGGCGGGGCTGTGCGCCTCC  664
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RESULT 27

BM546362/c

LOCUS BM546362 687 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6498563 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5722924 5', mRNA sequence.
ACCESSION BM546362
VERSION BM546362.1 GI:18779258
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Invitrogen
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM12709 row: m column: 05
  High quality sequence stop: 616.
FEATURES Location/Qualifiers
  source 1..687
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="IMAGE:5722924"
           /lab_host="DH10B"
           /clone_lib="NIH_MGC_125"
           /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
           Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
           of three ovaries, from females ranging in age from 38 to

---

```
Db                  49 yo. Library is oligo-dT primed and directionally cloned
                       (EcoRV site is destroyed upon cloning). Average insert
                       size 2.1 kb. insert size range 1-3.5 kb. Library is
                       normalized and enriched for full-length clones and was
                       constructed by C. Gruber (Invitrogen). Research Genetics
                       tracking code 036."

ORIGIN

Query Match        52.5%;  Score 629;  DB 4;  Length 687;
Best Local Similarity  99.8%;  Pred. No. 6.5e-143;
Matches  640;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy     1  GGAACTAAAAAAGAAC-TTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCA   59
             |||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db   661  GGAACTAAAAAAGAACTTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCA   602
Qy    60  AAAGCTTATCTGTATTTAACTTTCTTTCTCTGCTTGTCAATGAGAGTTAGATTTTAT   119
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AAAGCTTATCTGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT   542
Qy   120  TTTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGG   179
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TTTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGG   482
Qy   180  GGCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT   239
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  GGCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT   422
Qy   240  TTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT   299
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TTCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT   362
Qy   300  GGTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTGCCATCTCTCACACTG   359
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GGTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTGCCATCTCTCACACTG   302
Qy   360  GTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCC   419
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCC   242
Qy   420  AGGGAACTCCTTTTCCATGAGTACTCTCCAGTCCTCCTTGTTAAGTAGCCTTTATCCCC   479
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  AGGGAACTCCTTTTCCATGAGTACTCTCCAGTCCTCCTTGTTAAGTAGCCTTTATCCCC   182
Qy   480  AGCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCAT   539
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AGCGAATTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCAT   122
Qy   540  TTTGGTGGTCCGTTGAAGCCTTGGCCGAGGCCGCGGACGGCGGGCGAGCTGGGCGA   599
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TTTGGTGGTCCGTTGAAGCCTTGGCCGAGGCCGCGGACGGCGGGCGAGCTGGGCGA   62
Qy   600  GCTGGACGCGGGGCGGGGCGGAGGCCGAGCCGCGGCGGGGCTGTGCG   640
             |||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GCTGGACGCGGGGCGGGGCGGAGGCCGAGCCGCGGCGGGGCTGTGCG   21
```

RESULT 28

BF686811/c

LOCUS BF686811 938 bp mRNA linear EST 22-DEC-2000
DEFINITION 602140775F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301946 5', mRNA sequence.
ACCESSION BF686811
VERSION BF686811.1 GI:11972219
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 938)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

```
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1163  row: e  column: 19
             High quality sequence stop: 654.
FEATURES             Location/Qualifiers
     source          1..938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4301946"
                     /tissue_type="leiomyosarcoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC 46"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library construced by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."

ORIGIN

Query Match         52.4%;    Score 628.6;    DB 2;    Length 938;
Best Local Similarity   99.2%;    Pred. No. 8.5e-143;
Matches  642;    Conservative    0;    Mismatches    4;    Indels    1;    Gaps    1;

Qy      1 GGAACTAAAAAAGAACTTATTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    648 GAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGTATGCAAACAATACCAAAATCAA 589

Qy     61 AAGCTTATCTGGTATTAACTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    588 AAGCTTATCTGGTATTTAACTTTTCTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTTATT 529

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    528 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG 469

Qy    181 GCAGATTCCTAAGCCACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    468 GCAGATTCCTAAGCCACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 409

Qy    241 TCTGCCTACTTCTTTCCCTTCGCTTCTTCATGTGTACTAC-AAAATAGTCATTGCATGCAAT 299
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    408 TCTGCCTACTTCTTTCCCTTCGCTTCTTCATGTGTACTACAAAAAATAGTCATTGCATGCAAT 349

Qy    300 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTTCGGAGCCCACTTTGCCATCTCTACACTG 359
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    348 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTCGGAGCCCACTTTTGCCATCTCTACACTG 289

Qy    360 GTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAATCC 419
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    288 GTCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAAATCC 229

Qy    420 AGGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCC 479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    228 AGGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCC 169

Qy    480 AGCGAATTTGTGAAATGTAAACATCATGGCGTGTTCCATTGAGATGGCAT 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    168 AGCGAATTTGTGAAATGTAAACATCATGGCGTGTTCCATTTTGAGATGGCAT 109

Qy    540 TTTGGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCCGACGCGTCGGGCGCA 49
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db      ...
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Db    108 TTTGGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCCGACGCGTCGGGCGCA 49

Qy    600 GCTGGACGCGGGGCGGGGGCGGCGGAGGCGAGGCGGCGGGGGCTGTGCGCGCCTTCC 646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     48 GCTGGACGCGGGGCGGGGGCGGCGGAGGCGAGGCGGCGGGGGCTGTGCGCGCCTTCC 2
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```
RESULT 29
BE745512/c
LOCUS       BE745512                990 bp    mRNA    linear    EST 15-SEP-2000
DEFINITION  601579889F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928606 5',
            mRNA sequence.
ACCESSION   BE745512
VERSION     BE745512.1  GI:10159504
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM760  row: a  column: 23
            High quality sequence stop: 650.
FEATURES             Location/Qualifiers
     source          1..990
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3928606"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC 9"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACCAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match         52.4%;    Score 628.6;    DB 2;    Length 990;
Best Local Similarity   99.4%;    Pred. No. 8.6e-143;
Matches  631;    Conservative    0;    Mismatches    4;    Indels    0;    Gaps    0;

Qy      1 GGAACTAAAAAAGAACTTATTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    635 GGAACTAAAAAAGAACTTTATTTATTATTGAGGGCAAGGGGATGCAAACAATACCAAAATCAA 576

Qy     61 AAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    575 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTTATT 516

Qy    121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    515 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGAAGCTGTGGG 456

Qy    181 GCAGATTCCTTAAGCCACCCTTGGACAACTCTTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    455 GCAGATTCCTTAAGCCACCCTTTGGACAACTCTTTATCAGGGAGGAGGAGCGAACTGCTCATT 396

Qy    241 TCTGCCTACTTCTTTCCCTTCGCTTCTTCATGTGTACTACAAAAATAGTCATTGCATGCAATG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    ...
```

Matches 651; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

```
Qy      1 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATAC-AAAAATCA  59
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    654 GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACGCAAAAATCA  595

Qy     60 AAAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT  119
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594 AAAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT  535

Qy    120 TTTTACATTTGCTAAGTGCTCCTGATCTGCTCATGCAAATCCTTCATGGGGAAGCTGTGG  179
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 TTTTACATTTGCTAAGTGCTCCTGATCTGCTCATGCAAATCCTTCATGGGGAAGCTGTGG  475

Qy    180 GGCAGATCCTTAAGCGACCCCTTTGGGACAACTTCATCAGGGAGGAGGGAACTGCTCAT  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474 GGCAGATTCCTTAAGCGACCCCTTTGGGACAACTTCATCAGGGAGGAGGGAACTGCTCAT  415

Qy    240 TTCTGCCTACTTCTTCCCTTCGTCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 TTCTGCCTACTTCTTCCCTTCGTCTTCATGTGTACTACAAAATAGTCATTGCATGCAAT  355

Qy    300 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACACTG  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    354 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACACTG  295

Qy    360 GTCCAGGTCCTTCATTATTTTGTCCACAGCCCAGAGGGGTCTTTTTGATTTTCCAAAAATCC  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 GTCCAGGTCCTTCATTATTTTGTCCACAGCCCAGAGGGGTCTTTTTGATTTTCCAAAAATCC  235

Qy    420 AGGGAACTCCTTTTCCATGAGTA-CTCTCAGGTGCCTCCTCCTTTGTTAAGTAGCCTTTATCCC  478
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    234 AGGGAACTCCTTTTCCATGAGTAGCTCTCAGGTGCCTCCTCCTTTGTTAAGTAGCCTTTATCCC  175

Qy    479 CAGCGAATTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCCATTGAGATGGCA  538
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    174 CAGCGAATTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCCATTGAGATGGCA  115

Qy    539 TTTTGGTGGTCCGTTGAAGCCTTGAAGCCTTGAAGCCTGGCGGCGGACGGCTGGGCAGCTGGGGG  598
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    114 TTTTGGTGGTCCGTTGAAGCCTTGAAGCCTGGCGGCGGACGGCTGGGCAGCTGGGGG  55

Qy    599 AGCTGGACGGCGGGCGGAGAGGCGAGCGGCGGCGGCGGCTGTGCGCCTTCCTTAGTA  652
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     54 AGCTGGACGGCGGGCGGAGAGGCGAGCGGCGGCGGCGGCTGTGCGCCTTCCTTAGTA   1
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RESULT 31
CA307888
LOCUS   CA307888   686 bp   mRNA   linear   EST 05-AUG-2004
DEFINITION   UI-H-FT1-bib-a-01-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
             UI-H-FT1-bib-a-01-0-UI 3', mRNA sequence.
ACCESSION   CA307888
VERSION   CA307888.1 GI:24470942
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 686)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
             from Dr. M. Bento Soares, bento-soares@uiowa.edu
             Seq primer: M13 FORWARD

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Db    395 TCTGCCTACTTCTTCCCTTCGTCTTCATGTGTGCTTACTACAAAATAGTCATTGCATGCAATG  336
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACACTGG  360

Db    335 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTCACACTAG  276

Qy    361 TCCAGGTCCTTCATTATTTTGTCCACAGCAGCCAGGGGTCTTTTTGATTTTCCAAAAATCCA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    275 TCCAGGTCCTTCATTATTTTGTCCACAGCAGCCAGGGGTCTTTTTGATTTTCCAAAAATCCA  216

Qy    421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    215 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  156

Qy    481 GGCAATTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCCATTTGAGATGGCATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 GGCAATTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCCATTTGAGATGGCATT  96

Qy    541 TTGGTGGTCCGTTGAAGCCTTGGCCGAGCACCGTGGGCAGCGGCGGGCGGCGGAGAGGCGGGCGAG  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     95 TTGGTGGTCCGTTGAAGCCTTGGCCGAGCACCGTGGGCAGCGGCGGGCGGCGGAGAGGCGGGCGAG  36

Qy    601 CTGGACGCGGGGCGGCGGAGAGGCGAGCGGCGGCGCGCGGGCT  635
            |||||||||||||||||||||||||||||||||||||||||
Db     35 CTGGACGCGGGGCGGCGGAGAGGCGAGCGGCGGCGCGCGGGCT  1
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RESULT 30
BI858258/c
LOCUS   BI858258   674 bp   mRNA   linear   EST 10-OCT-2001
DEFINITION   603384021F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5392973 5',
             mRNA sequence.
ACCESSION   BI858258
VERSION   BI858258.1 GI:15999005
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 674)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM12001 row: i column: 06
             High quality sequence stop: 663.
FEATURES   Location/Qualifiers
     source   1..674
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5392973"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_87"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

Query Match   52.4%;   Score 628.4;   DB 4;   Length 674;
Best Local Similarity 99.5%;   Pred. No. 9.1e-143;

```
Db   319  GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG  378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA  438
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421  GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA    480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439  GGGAACTCCTTTCCATGAGTACTCCAGGTCCTCCTTGTTAAGTAGCCTTTATCCCCA    498
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481  GCGAATTGTGAAATGTAAAACATCATGGTTCCATGGCGTGTTCCATTGAGATGGCATT  540
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   499  GCGAATTGTGAAATGTAAAACATCATGGTTCCATGGCGTGTTCCATTGAGATGG-ATT  557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACCTGGGCGAGCTGGGCGGCAG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   558  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACCTGGGCGAGCTGGGCGGCAG  617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601  CTGGACGCGGGGCGGGAGAGGCGAGCGCGGGGCGGGGCTGTGCGCCTTCCTTAGTACGTGC  657
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   618  CTGGACGCGGGGCGGGCGGAAAGGCGCAGCGCGGGGCGGGGCTGTGCG-CTTCCTTAGTACGTCC  673
```

RESULT 32
BI488419/c

LOCUS   BI488419   811 bp   mRNA   linear   EST 28-AUG-2001
DEFINITION 603020917F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191564 5',
            mRNA sequence.
ACCESSION   BI488419
VERSION   BI488419.1   GI:15327647
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 811)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11479 row: a column: 05
            High quality sequence stop: 669.
FEATURES   Location/Qualifiers
     source   1..811
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5191564"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_114"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
ORIGIN

Query Match   52.4%;   Score 627.8;   DB 4;   Length 811;
Best Local Similarity 98.2%;   Pred. No. 1.3e-142;
Matches 659;   Conservative   0;   Mismatches   2;   Indels 10;   Gaps   2;

```
                                                                     FEATURES             source          POLYA=Yes.
                                                                                                          Location/Qualifiers
                                                                                                          1..686
                                                                                                          /organism="Homo sapiens"
                                                                                                          /mol_type="mRNA"
                                                                                                          /db_xref="taxon:9606"
                                                                                                          /clone="UI-H-F71-bib-a-01-0-UI"
                                                                                                          /tissue_type="Alveolar Macrophage"
                                                                                                          /dev_stage="Adult"
                                                                                                          /lab_host="DH10B (Life Technologies)"
                                                                                                          /clone_lib="NCI_CGAP_F71"
                                                                                                          /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                                                                                                          modified polylinker; Site_1: EcoR I; Site_2: Not I;
                                                                                                          NCI_CGAP_F71 is a normalized cDNA library constructed from
                                                                                                          a pool of 81 RNA samples from Alveolar Macrophages
                                                                                                          challenged with different treatments. The mRNA samples
                                                                                                          were a mixture of these conditions (times refer to
                                                                                                          incubations following isolation by bronchoalveolar lavage)
                                                                                                          (some normal donor macrophages were cultured in some of
                                                                                                          the conditions, other donor macrophages in different
                                                                                                          conditions). The mRNA samples were pooled for library
                                                                                                          construction. Control 0 hours; control 3 hours; control 24
                                                                                                          hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours;
                                                                                                          PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella
                                                                                                          moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                                                                                                          moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                                                                                                          vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                                                                                                          (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                                                                                                          3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                                                                                                          3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                                                                                                          hours; wt adenovirus + LPS 24 hours. The library was
                                                                                                          normalized according to Bonaldo, Lennon and Soares, Genome
                                                                                                          Research, 6:791-806, 1996. First strand cDNA synthesis was
                                                                                                          primed with an oligo-dT primer containing a Not I site.
                                                                                                          Double stranded cDNA was ligated to an EcoR I adaptor,
                                                                                                          digested with Not I, and cloned directionally into
                                                                                                          pT7T3-Pac vector. The oligonucleotide used to prime the
                                                                                                          synthesis of first-strand cDNA contains a library tag
                                                                                                          sequence that is located between the Not I site and the
                                                                                                          (dT)18 tail. The sequence tag for this library is
                                                                                                          GGCCATGCCG. The tissue was provided by Dr. Gary W.
                                                                                                          Hunninghake of the University of Iowa.
                                                                                                          TAG_TISSUE=Human Lung Alveolar Macrophage
                                                                                                          TAG_LIB=UI-H-F71
                                                                                                          TAG_SEQ=GGCCATGCCG"
                                                                     ORIGIN

                                                                     Query Match          52.4%;    Score 628.2;    DB 6;    Length 686;
                                                                     Best Local Similarity 99.2%;    Pred. No. 1e-142;
                                                                     Matches 652;    Conservative   0;    Mismatches   3;    Indels   2;    Gaps   2;

Qy     1  GGAACTAAAAAGAAGAACTTTATTTATTGAGGGGAAGGGGATGCAAACAATACAAAAATCAA   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19  GGAACTAAAAAGAAGAACTTTATTTATTGAGGGGAAGGGGATGCAAACAATACAAAAATCAA   78
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61  AAGCTTATCTGGTATTTAACTTTTCTTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    79  AAGCTTATCTGGTATTTAACTTTTCTTTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121  TTTACATTTGCTCAAGTGTCCTGATCTGCTCATCGTCCTGATGAAATCCTTCTATGGGGAAGCCTGTGGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139  TTTACATTTGCTCAAGTGTCCTGATCTGCTCATCGTCCTGATGAAATCCTTCTATGGGGAAGCCTGTGGG  198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181  GCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199  GCAAATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATT  258
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241  TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259  TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG  318
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301  GTGAGGGCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES　　　　Location/Qualifiers
　source　　　　1..665
　　　　　　　　/organism="Homo sapiens"
　　　　　　　　/mol_type="mRNA"
　　　　　　　　/db_xref="taxon:9606"
　　　　　　　　/clone="UI-H-EZ0-bak-j-10-0-UI"
　　　　　　　　/tissue_type="Chondrosarcoma Grade II"
　　　　　　　　/dev_stage="Adult"
　　　　　　　　/lab_host="DH10B (Life Technologies)"
　　　　　　　　/clone_lib="NCI_CGAP_Ch1"
　　　　　　　　/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
　　　　　　　　with a modified polylinker; Site_1: EcoR I; Site_2: Not I.
　　　　　　　　NCI_CGAP_Ch1 is a cDNA library containing the following
　　　　　　　　tissue(s): Chondrosarcoma Grade II. The library was
　　　　　　　　constructed according to Bonaldo, Lennon and Soares,
　　　　　　　　Genome Research, 6:791-806, 1996. First strand cDNA
　　　　　　　　synthesis was primed with an oligo-dT primer containing a
　　　　　　　　Not I site. Double stranded cDNA was ligated to an EcoR I
　　　　　　　　adaptor, digested with Not I, and cloned directionally
　　　　　　　　into pT7T3-Pac vector. The oligonucleotide used to prime
　　　　　　　　the synthesis of first-strand cDNA contains a library tag
　　　　　　　　sequence that is located between the Not I site and the
　　　　　　　　(dT)18 tail. The sequence tag for this library is
　　　　　　　　TGATCACGCT.
　　　　　　　　TAG_TISSUE=grade-2-chondrosarcoma
　　　　　　　　TAG_LIB=UI-H-EZ0
　　　　　　　　TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match　　　52.3%;　　Score 627;　DB 6;　Length 665;
Best Local Similarity　99.1%;　Pred. No. 2e-142;
Matches 641;　Conservative　0;　Mismatches　5;　Indels　1;　Gaps　1;

Qy　　1 GGAACTAAAAAGAACTTTATTTAT-TGAGGGCAAGGGGATGCAAACAATACAAAAATCA 59
　　　　|||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db　 19 GGAACTAAAAAGAACTTTATTTATNTGAGGGCAAGGGGATGCAAACAATACAAAAATCA 78

Qy　 60 AAAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT 119
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　 79 AAAGCTTATCTGGTATTTAACTTTCTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT 138

Qy　120 TTTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCAGGGAGGAAGCTGTGG 179
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　139 TTTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCAGGGAGGAAGCTGTGG 198

Qy　180 GGCAGATTCCTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT 239
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　199 GGCAGATTCCTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT 258

Qy　240 TTCTGCCACTCTTCTTTCCCTTCGCTTCTTATTTATTNTGAGGCATACAAAATCAAAAATCA 299
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　259 TTCTGCCACTCTTCTTTCCCTTCGCTTCTTATTTATTNTGAGGCATACAAAATCAAAAATCA 318

Qy　300 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAAAGAAGCTCTGGAAGCCCACTTG 359
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　319 GGTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAAAGAAGCTCTGGAAGCCCACTTG 378

Qy　360 GTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCC 419
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　379 GTCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTCCAAAAATCC 438

Qy　420 AGGGAACCCCTTTCCATGAGTACTCCAGGTCCTCCTTCGTTTAAGTAGCCTTTATCCCC 479
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　439 AGGGAACCCCTTTCCATGAGTACTCCAGGTCCTCCTTCGTTTAAGTAGCCTTTATCCCC 498

Qy　480 AGCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCAT 539
　　　　||||||||||||||||||||||||||||||||||||||||||||||
Db　499 AGCGAATTTGTGAAATGTAAACATCATGGTTCCATTGAGATGGCAT 558

Qy　540 TTTGGTGTGGTCCGTTGAAGCCTTGGAGCGCGCGGAC--------GCTGGGCGA 590
　　　　|||||||||||||||||||||||||||||||||||| ||||||||
Db　131 TTTGGTGTGGTCCGTTGAAGCCTTGGAGCGCGCGGACGCGCGGGGCGAGCTGGGCGA 72

Qy　591 GCTGGGGCGAGCTGGACGCGGGGCGGAGAGGCCAGAGGCGCGGGGCGTGCGCCTTCCTTAG 650
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　 71 GCTGGGGCGAGCTGGACGCGGGGCGGAGAGGCCAGAGGCGCGGGGCGTGCGCCTTCCTTAG 12

Qy　651 TACGTGCGGCG 661
　　　　|||||||||||
Db　 11 TACGTGCGGCG 1

RESULT 33
CA412335
LOCUS　　　　CA412335　　　　 665 bp　 mRNA　　 linear　 EST 07-NOV-2002
DEFINITION　UI-H-EZ0-bak-j-10-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone
　　　　　　　UI-H-EZ0-bak-j-10-0-UI 3', mRNA sequence.
ACCESSION　 CA412335
VERSION　　 CA412335.1　GI:24774986
KEYWORDS　　EST.
SOURCE　　　Homo sapiens (human)
　ORGANISM　Homo sapiens
　　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　　Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　 1 (bases 1 to 665)
AUTHORS　　 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
TITLE　　　 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
　　　　　　　Tumor Gene Index
JOURNAL　　 Unpublished (1997)
COMMENT　　 Contact: Robert Strausberg, Ph.D.
　　　　　　　Email: cgapbs-r@mail.nih.gov
　　　　　　　Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
　　　　　　　Orthoapedics
　　　　　　　cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
　　　　　　　cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
　　　　　　　DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

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Qy    540  TTTGGTGTGGTCCGTTGAAGCCTTGGCCGAGCGCGCGGCGCGGCGCGAGCTGGGCGA  599
           ||||||||||||||||||||||||||||| |||||||  ||| |||||||||||||||
Db    559  TTTGGTGTGGTCCGTTGAAGCCTTGTGTGCGAGCGGCGGCGCGCTGGGGATCTGGGCGA  618

Qy    600  GCTGGACGCGGCGGGGCGAGAGGCGCAGCGGCGGGGGGCTGTGCGCCTTCC  646
           |||||||||  ||| |||  ||| |||||||||||||||||||||||||||
Db    619  GCTGGACCCGGAGCCGAGCCGAGCCGAGCGCGCGGGGGCTGTGCGCCTTCC  665


RESULT 34
AI749536
LOCUS       AI749536                    641 bp    mRNA    linear    EST    22-JUN-1999
DEFINITION  at30b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
            IMAGE:2373491 3' similar to gb:M38591 CALPACTIN I LIGHT CHAIN
            (HUMAN), mRNA sequence.
ACCESSION   AI749536
VERSION     AI749536.1  GI:5127800
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 641)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
  COMMENT   Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 470.
FEATURES             Location/Qualifiers
     source          1..641
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2373491"
                     /sex="male"
                     /dev_stage="adult, age 25"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Barstead colon HPLRB7"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
                     strand cDNA was primed with a NotI - oligo(dT) primer [5'
                     TGTTACGGAATCTGAAGTGGAGCCGGCCGCCCTCTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     [5' AATTCACTACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested
                     with Not I and cloned into the Not I and Eco RI sites of
                     the modified pT7T3 vector. Library constructed by Bob
                     Barstead."
ORIGIN

Query Match             52.2%;  Score 626.4;  DB 1;  Length 641;
Best Local Similarity   98.7%;  Pred. No. 2.8e-142;
Matches   630;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      1  GGAACTAAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA   60
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      4  GGAACTAAAATAGAACTTTATTTATTTATTGAGGGCAAGGGGCAAGGGGGCGAACAATACAAAAATCAA   63

Qy     61  AAGCTTATCTGGTATTAACTTTTCTTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64  AAGCTTATCTGGTATTTAACTTTTCTTTTCTTTTCTGCTTGTCAAATGAGAGTTAGATTTTATT  123

Qy    121  TTTACATTTGCTAAGTGTCCTGATCGTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  180
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Db    124  TTTACATTTGCTAAGTGTCCTGATCGTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG  183
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    181  GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGAGGAGGAGCGAACTGCTCATT  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184  GCAGATTCCTTAAGCGACCCTTTGGACAACTCTTATCAGGAGGAGGAGCGAACTGCTCATT  243

Qy    241  TCTGCCTACTTCTTCCCTTCGTTCCTTTCGTTCCTTTCGTTCCTTTCGTTGTACTACAAAATAGTCATTGCATGCAATG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244  TCTGCCTACTTCTTCCCTTCGTTCCTTTCGTTCCTTTCGTACTACAAAATAGTCATTGCATGCAATG  303

Qy    301  GTGAGGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304  GTGAGGGCCCGCAATTAGGAAAAGAAGCTCTGGAAGCCCACTTGCCATCTCACACTGG  363

Qy    361  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364  TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA  423

Qy    421  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424  GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA  483

Qy    481  GCGAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484  GCGAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT  543

Qy    541  TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGCGCGCGGCGACCGCTGGGCGAGCTGGGCGAG  600
           |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Db    544  NTGGTGTGGTCCGTTGAAGCCTTGGCCGAGCGCGCGGCGAGCGCGCGGCGAGCTGGGCGAG  603

Qy    601  CTGGACGCGGGGGCGGAGAGGCGAGCGGCGCGGCGGCTGTG  638
           ||||||||||| ||||||||||||| ||||||||||||||
Db    604  CTGGACGCGGNCGCGAGAGGCGAGCGGCGCGGCGGCTGTG  641


RESULT 35
BQ948995/c
LOCUS       BQ948995                    641 bp    mRNA    linear    EST    21-AUG-2002
DEFINITION  AGENCOURT_8912008 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6464957
            5', mRNA sequence.
ACCESSION   BQ948995
VERSION     BQ948995.1  GI:22364473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 641)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13986  row: o  column: 06
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6464957"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC 71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
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cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11029 row: n column: 18
High quality sequence stop: 671.

FEATURES   Location/Qualifiers
     source   1..697
                  /organism="Homo sapiens"
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                  /db_xref="taxon:9606"
                  /clone="IMAGE:4999505"
                  /cell_line="MGC36"
                  /lab_host="DH10B"
                  /clone_lib="NIH_MGC_10"
                  /note="Organ: cervix; Vector: pCMV-SPORT6, Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.5 kb. Library prepared by Life
                  Technologies."

ORIGIN

Query Match   52.1%;   Score 625; DB 4; Length 697;
Best Local Similarity 95.9%; Pred. No. 6.2e-142;
Matches 653; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

Qy   8 AAAAAGAACTTATTATTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAAAAGCTTA 67
            ||||||| |||||||||||||||||||||||||||| ||||||| || ||||||||||
Db   678 AACTAAAAGAACTTATTTATTTGAGGGCAAGGGGATGCGCAAAC---ATACAGAATCAAAGCTTA 622

Qy   68 TCTGGTATTTAACTTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTATTTTACAT 127
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   621 TCTGGTATTTAACTTGTCCTTCTTCTCGCTTGTCAAATGAGAGTTAGATTTTGATTTTGACAT 562

Qy   128 TTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGGCAGATT 187
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 TTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGGCAGATT 502

Qy   188 CCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCT 247
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 CCTTAAGCGACCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATTTCTGCCT 442

Qy   248 ACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGC 307
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 ACTTCGTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGC 382

Qy   308 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGT 367
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 CCGCAATTAGGGAAAAGAAGCTCTGGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGT 322

Qy   368 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCAGGGAACT 427
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 CCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCAAAAATCCAGGGAACT 262

Qy   428 CCTTTTCCATGAGTACTCTCAGGTCCTCCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCAGCGAATT 487
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 CCTTTTCCATGAGTACTCTCAGGTCCTCCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCAGCGAATT 202

Qy   488 TGTGAAATGTAAACATCATGGTTTCCATTGGATGGCATTTGGTGT 547
            ||||||||||||||||||||||||||||||||||||||||||
Db   201 TGTGAAATGTAAACATCATGGTTTCCATTGGATGGCATTTGGTGT 142

Qy   548 GGTCCGTTGAAGCTTGGGGCCGGAGGCGCCGGACGCTGGGCGAGCTGGACG 607
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 GGTCCGTTGAAGCCTTGGGGCCGGAGGCGCCGGACGCTGGGCGAGCTGGACG 82

Qy   608 CGGGGCGGAGAGGCGAGCGCGCGGGGGTCGGCGTGCGCCTTCCTTAGTACGTGCGGGGTGGG 667
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 CGGGGCGGAGAGGCGAGCGCGCGGGGGTCGGCGTGCGCCTTCCTTAGTACGTGCGGGGTGGG 22

Qy   668 TAGAGGGAGGCGCGCGCGGGAG 688
            |||||||||||||||||||
Db   21 TAGAGGGAGGCGGGTGCGGGAG 1

RESULT 36
BI093074/c
LOCUS   BI093074   697 bp   mRNA   linear   EST 20-JUN-2001
DEFINITION 602S8171F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4999505 5',
            mRNA sequence.
ACCESSION   BI093074
VERSION   BI093074.1   GI:14511404
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 697)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.

ORIGIN

            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 2.1 kb. "

Query Match   52.1%;   Score 625; DB 5; Length 641;
Best Local Similarity 100.0%; Pred. No. 6.1e-142;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
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Db   625 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 566

Qy   61 AAGCTTATCTGGTATTTAACTTTCTTCTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 AAGCTTATCTGGTATTTAACTTTCTTCTCTCGCTTGTCAAATGAGAGTTAGATTTTATT 506

Qy   121 TTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 TTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGGG 446

Qy   181 GCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 GCAGATTCCTTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 386

Qy   241 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 TCTGCCTACTTCTTTCCCTTCGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 326

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 266

Qy   361 TCCAGGTCCTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 TCCAGGTCCTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 206

Qy   421 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCA 480
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Db   205 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCCTCCTTGTTAAGTAGCCTTATCCCCA 146

Qy   481 GGGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGATGGCATT 540
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Db   145 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATTGGATGGCATT 86

Qy   541 TTGGTGTGGTCCGTTGAAGCCTTGGGGCCGGAGGCGCCGGACGCGCTGGGCGAGCTGGGGCGAG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85 TTGGTGTGGTCCGTTGAAGCCTTGGGGCCGGAGGCGCCGGACGCGCTGGGCGAGCTGGGGCGAG 26

Qy   601 CTGGACGCGGGGCGGGGGGCGGAGAGGCGAGC 625
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Db   25 CTGGACGCGGGGCGGGGGGCGGAGAGGCGAGC 1

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RESULT 37
CN271600/c
LOCUS       CN271600               637 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  1700060075087 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN271600
VERSION     CN271600.1  GI:47288014
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
  COMMENT   Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 637   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1..637
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cell, retinoic acid and
                     mitogen-treated hES cell line H7"
                     /clone_lib="GRN_PRENEU"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from hES cell line H7 (p29) maintained in feeder-free
                     conditions. Embryoid bodies were generated in the presence
                     of all-trans retinoic and mitogens."
ORIGIN

Query Match    51.9%;   Score 622.8;  DB 7;  Length 637;
Best Local Similarity  99.7%;   Pred. No. 2.1e-141;
Matches  624;   Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy      1 GGAACTAAAAAAGAACTTATTTATTGAGGCAAGGGATGCAAACAATACAAAAATCAA  60
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Db    626 GGAACTAAAAAAGAACTTATTTATTGAGGCAAGGGATGCAAACAATACAAAAATCAA 567

Qy     61 AAGCTTATCTGGTATTAACTTCCCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    566 AAGCTTATCTGGTATTAACTTCCCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 507

Qy    121 TTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
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Db    506 TTTACATTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 447

Qy    181 GCAGATTCCTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT 240
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Db    446 GCGAGATTCCTAAGCGACCCCTTGGGACAACTCTTATCAGGGAGGAGGCGAACTGCTCATT 387

Qy    241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    386 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 327

Qy    301 GTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    326 GTGAGGCCCGCAATTAGGGAAAAGAAGAGCTCTGGAAGCCCACTTGCCATCTCTACACTGG 267

Qy    361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    266 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGGAGGGTCTTTTTGATTTTCCAAAAATCCA 207
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Qy    421 GGGAACTCCTTTTCCATGAGTACTCCTTCCTTTGTAAGTAGCCTTTATCCCCA 480
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Db    206 GGGAACTCCTTTTCCATGAGTACTCCTTCCTTTGTAAGTAGCCTTTATCCCCA 147

Qy    481 GCGAATTTGTGAAATGTAAACATCATGGTGTTCCATTGAGGTGTGTTCCATTGGCATT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    146 GCGAATTTGTGAAATGTAAACATCATGGTGTTCCATTGAGGTGTGTTCCATTGGCATT 87

Qy    541 TTGGTGTGTCCGTTGGAAGCCTTGGCCGGAGGCGCGGCGCGACCTGGGCGAGCTGGGCGAG 600
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Db     86 TTGGTGTGTCCGTTGGAAGCCTTGGCCGGAGGCGCGGCGCGACCTGGGCGAGCTGGGCGAG 27

Qy    601 CTGGACGCGGGGCGCGGAGGCGCGAGCG 626
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Db     26 CTGGACGCGGGGCGCGGAGAGGCGCGACG 1
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RESULT 38
BM767559/c
LOCUS       BM767559               625 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0050042 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-3-G06 5',
            mRNA sequence.
ACCESSION   BM767559
VERSION     BM767559.1  GI:19097174
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 625)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
  COMMENT   Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 3  row: G  column: 06
            High quality sequence stop: 625.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S1SNU5s2-3-G06"
                     /sex="F"
                     /tissue_type="Ascites"
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                     /lab_host="Top10F'"
                     /clone_lib="S1SNU5s2"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library. After analyzing and
```

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 628)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE   21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 56 row: F column: 10
            High quality sequence stop: 628.
FEATURES   Location/Qualifiers
     source   1..628
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S12SNU216-56-F10"
                     /sex="F"
                     /tissue_type="lymph node"
                     /cell_type="Epithelial"
                     /cell_line="SNU-216"
                     /lab_host="Top10F'"
                     /clone_lib="S12SNU216"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tobacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."

ORIGIN

Query Match   51.8%;   Score 621.4; DB 4; Length 628;
Best Local Similarity 99.8%; Pred. No. 4.7e-141;
Matches 622; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAA 60
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Db   623 GGAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAAATCAA 564

Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTTCTTTCTTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db   563 AAGCTTATCTGGTATTTAACTTTTCTTTTCTTTCTTGCTTGTCAAATGAGAGTTAGATTTTATT 504

Qy   121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAGGGAAGCTGTGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAGGGAAGCTGTGG 444

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   443 GCAGATTCCTTAAGCGACCCTTTGGGACAACCTTATCAGGGAGGAGGAGCGAACTGCTCATT 384

Qy   241 TCTGCCTACTTCTTTCCCTTCGTTGCTTCATGTGTACTACAAAAATAGTCATTGCATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   383 TCTGCCTACTTCTTTCCCTTCGTTGCTTCATGTGTACTACAAAAATAGTCATTGCATG 324

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360

ORIGIN

kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

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Query Match         51.8%;  Score 621;  DB 5;  Length 794;
Best Local Similarity  100.0%;  Pred. No. 6e-141;
Matches  621;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
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Db  624 GGAACTAAAAAGAACTTATTTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 565

Qy   61 AAGCTTATCTGTATTTAACTTTCTTTCTCTGTCAAATGAGAGTTAGATTTTATT 120
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Db  564 AAGCTTATCTGTATTTAACTTTCTTTCTCTGTCAAATGAGAGTTAGATTTTATT 505

Qy  121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  504 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 445

Qy  181 GCAGATTCCTTAAGCACCCTTTGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  444 GCAGATTCCTTAAGCACCCTTTGGACAACTCTTATCAGGGAGGAGGAGCGAACTGCTCATT 385

Qy  241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  384 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 325

Qy  301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACTGG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  324 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACTGG 265

Qy  361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGGTCTTTTTGATTTTCCAAAAATCCA 420
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Db  264 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGGTCTTTTTGATTTTCCAAAAATCCA 205

Qy  421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  204 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 145

Qy  481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
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Db  144 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 85

Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGCGGCCGGGACGCTGGGCGAGCTGGGGCGAG 600
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Db   84 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGCGGCCGGGACGCTGGGCGAGCTGGGGCGAG 25

Qy  601 CTGGACGCGGGGCGGAGAGGC 621
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Db   24 CTGGACGCGGGGCGGAGAGGC 4
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RESULT 41
BQ943717/c
LOCUS   BQ943717   638 bp   mRNA   linear   EST 21-AUG-2002
DEFINITION AGENCOURT_8777162 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6384795
            5', mRNA sequence.
ACCESSION   BQ943717
VERSION   BQ943717.1 GI:22359195
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 638)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov

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Db  323 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACTGG 264
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGGTCTTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  263 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGGTCTTTTTGATTTTCCAAAAATCCA 204

Qy  421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
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Db  203 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 144

Qy  481 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143 GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 84

Qy  541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGCGGCCGGGACGCTGGGCGAGCTGGGGCGAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 TTGGTGTGGTCCGTTGAAGCCTTGGCCGGCGGCCGGGACGCTGGGCGAGCTGGGGCGAG 24

Qy  601 CTGGACGCGGGGCGGAGAGGCGGA 623
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Db   23 CTGGACGCGGGGCGGAGAGGCTA 1
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RESULT 40
BU860855/c
LOCUS   BU860855   794 bp   mRNA   linear   EST 16-OCT-2002
DEFINITION AGENCOURT_10435041 NIH_MGC_126 Homo sapiens cDNA clone
            IMAGE:6652090 5', mRNA sequence.
ACCESSION   BU860855
VERSION   BU860855.1 GI:24045847
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 794)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: NCI
            cDNA Library Preparation: Michael Brownstein Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2899 row: p column: 10
            High quality sequence stop: 589.
FEATURES   Location/Qualifiers
     source   1..794
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6652090"
                     /tissue_type="mixed (pool of 40 RNAs)"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_126"
                     /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
                     Site 2: SfiI (ggccgcctcggcc); Double-stranded cDNA was
                     prepared from a pool of 40 cell line polyA+ RNAs (bladder
                     - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
                     4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
                     kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
                     5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
                     salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
                     adaptors were used in cloning as follows:
                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
                     enriched library was constructed using the Clontech
                     Creator SMART kit and size-selected to contain the 0.5-1

Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2580 row: g column: 04
High quality sequence stop: 637.

FEATURES
source   Location/Qualifiers
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              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:6384795"
              /tissue_type="carcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_40"
              /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
              Site_2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Library constructed by
              Ling Hong in the laboratory of Gerald M. Rubin (University
              of California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC Library."

ORIGIN

Query Match   51.7%; Score 620; DB 5; Length 638;
Best Local Similarity 100.0%; Pred. No. 1e-140;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
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Db 620 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 561

Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
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Db 560 AAGCTTATCTGGTATTTAACTTTTCTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 501

Qy 121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 500 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 441

Qy 181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGGAGGGAGCTGCTCATT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 440 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGGAGGGAGCTGCTCATT 381

Qy 241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 380 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 321

Qy 301 GTGAGGGCCGCAATTAGGGAAAGAAGCTCTGAAGCCCACTTTGCCATCTCTACACTGG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 320 GTGAGGGCCGCAATTAGGGAAAGAAGCTCTGAAGCCCACTTTGCCATCTCTACACTGG 261

Qy 361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 420
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Db 260 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTTGATTTTCCAAAAATCCA 201

Qy 421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
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Db 200 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 141

Qy 481 GCGAATTTGTGAAATGTAAACATCATGGTGTTCCATTTGAGATGGCATT 540
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Db 140 GCGAATTTGTGAAATGTAAACATCATGGTGTTCCATTTGAGATGGCATT 81

Qy 541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCCTGGCCGGCGGCGGGGAG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 TTGGTGTGGTCCGTTGGCCCAGGCCGGCGGCGGGACCGCTGGGCGAGCTGG 21

Qy 601 CTGGACGCGGGGCGGGAGAGG 620
        |||||||||||||||||||||
Db   20 CTGGACGCGGGGCGGGAGAGG 1

RESULT 42
BM461859/c
LOCUS   BM461859   AGENCOURT_6418411 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5533915
                       898 bp   mRNA   linear   EST 05-FEB-2002
DEFINITION AGENCOURT_6418411 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5533915
            5', mRNA sequence.
ACCESSION   BM461859
VERSION   BM461859.1 GI:18510899
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 898)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12219 row: i column: 20
            High quality sequence stop: 625.

FEATURES
source   Location/Qualifiers
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              /db_xref="taxon:9606"
              /clone="IMAGE:5533915"
              /tissue_type="leiomyosarcoma"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_71"
              /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
              Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
              Average insert size 2.1 kb. "

ORIGIN

Query Match   51.7%; Score 620; DB 4; Length 898;
Best Local Similarity 100.0%; Pred. No. 1.1e-140;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 60
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Db 620 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGATGCAAACAATACAAAAATCAA 561

Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 560 AAGCTTATCTGGTATTTAACTTTTCTTTCTTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 501

Qy 121 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 500 TTTACATTTGCTAAGTGTCCTGATCTGCTCATGAAATCCTTCATGGGGGAAGCTGTGGG 441

Qy 181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGGAGGGAGCTGCTCATT 240
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Db 440 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGGAGGGAGCTGCTCATT 381

Qy 241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 380 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGCATGCAATG 321

Qy 301 GTGAGGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 320 GTGAGGGCCCGCAATTAGGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 261

Qy   CTGGACGCGGGGCGGGAGAGG 620

Qy 361 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 260 TCCAGGTCCTTCATTATTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 201

Qy 421 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 200 GGGAACTCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA 141

Qy 481 GCGAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 140 GCGAATTGTGAAATGTAAACATCATGGTTTCCATGGCGTGTTCCATTTGAGATGGCATT 81

Qy 541 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGCGAG 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 80 TTGGTGTGGTCCGTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGCGAG 21

Qy 601 CTGGACGCGGGGCGGAGAGG 620
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Db 20 CTGGACGCGGGGCGGAGAGG 1

RESULT 43
BG335338/c
LOCUS   BG335338   645 bp   mRNA   linear   EST 27-FEB-2001
DEFINITION 602404165F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541488 5',
            mRNA sequence.
ACCESSION   BG335338
VERSION   BG335338.1   GI:13141776
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 645)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1220 row: b column: 17
            High quality sequence stop: 635.
FEATURES   Location/Qualifiers
     source   1..645
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4541488"
                     /tissue_type="choriocarcinoma"
                     /clone_lib="NIH_MGC_21"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites-selected by
                     following 5' adaptor: GGACGAG(G). cDNA synthesis kit
                     for average insert size 1.8kb. Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Query Match   51.7%; Score 619.8; DB 4; Length 645;
Best Local Similarity   98.6%; Pred. No. 1.2e-140;
Matches 636; Conservative   0; Mismatches   7; Indels   2; Gaps   1;

Qy 253 TTTCCCTTCTGCTTCATGTGTACTACCAAAATAGTCAATTGCATGCAATGGTGAGGCCCGCA 312
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Db 643 TTCCGCTTCTGCTTCATGTGTACTACCAAATAGTCATTGCATGCAATGTGA--GCCGCA 586
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Qy 313 ATTAGGGAAAAGAAGCTCTGGAAGCCACCTTTGCCATCTCACACTGGTCCTTCCTTC 372
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 585 ATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTC 526

Qy 373 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 432
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 525 ATTATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAATCCAGGGAACTCCTTT 466

Qy 433 TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 492
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Db 465 TCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTGTGA 406

Qy 493 AATGTAAACATCATGGTTTCCATTGCGGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 552
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Db 405 AATGTAAACATCATGGTTTCCATTGCGGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCC 346

Qy 553 GTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGCGGCGGGTGGGTAGAG 612
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 345 GTTGAAGCCTTGGCCGAGGCGGCGGACGCTGGGCGAGCTGGGCGGCGGGTGGGTAGAG 286

Qy 613 CGGAGAGGCGGCGAGCGCGGGAGGGAGAGGCGGGCGCTCGGCGGCCGCTCGGAGGGCCGCCC 672
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Db 285 CGGAGAGGCGAGCGCGGGCGGTGCGCGGGGCGCTCGGCGGCCGCTCGGAGGGCCGCCC 226

Qy 673 GGAGGGCGGCGGGAGGGGAGGAGCCTCGGGGCGCTCGGCGGCGCTCCCCAGCCCCACGCCC 732
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Db 225 GGAGGGCGGTGCGGGAGCGGGAGGAGCCTCGGGCGCTCGGCGGCGCTCCCCAGCCCCACGCCC 166

Qy 733 TGTCTCCTCCCCTCTTCCTGCCCCCGCCCCCGACTCCCCGGGGCCCACCCCCACGCCC 792
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Db 165 TGTCTCCTCCCCTCTTCCTGCCCCCGCCCCCGACTCCCCGGGGCCCACCCCCACGCCC 106

Qy 793 TGCCCTCGCTCCCGGACCCGCCTCGGCGAGAGGCCTCGCCCGCCCGCCCCCGACACAGAGCGTTCTTG 852
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RESULT 44
BU934696/c
LOCUS   BU934696   662 bp   mRNA   linear   EST 18-OCT-2002
DEFINITION AGENCOURT_10520015 NIH_MGC_128 Homo sapiens cDNA clone
            IMAGE:6701084 5', mRNA sequence.
ACCESSION   BU934696
VERSION   BU934696.1   GI:24123515
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 662)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: NCI
            cDNA Library Preparation: Michael Brownstein Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2991 row: i column: 20
            High quality sequence stop: 537.
FEATURES   Location/Qualifiers
     source   1..662
                     /organism="Homo sapiens"

RESULT 45

CB15822/c

LOCUS   CB158822   619 bp   mRNA   linear   EST 30-JAN-2003
DEFINITION   K-EST0218240 L18POOLln1 Homo sapiens cDNA clone L18POOLln1-27-A04
               5', mRNA sequence.
ACCESSION   CB158822
VERSION   CB158822.1 GI:28144948
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 619)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
               Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
               Kim,Y.S.
  TITLE   21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
               Genome Research Center
               Korea Research Institute of Bioscience & Biotechnology
               52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
               Tel: +82-42-860-4470
               Fax: +82-42-860-4409
               Email: yongsung@mail.kribb.re.kr
               Plate: 27 row: A column: 04
               High quality sequence stop: 619.
FEATURES   Location/Qualifiers
     source   1..619
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L18POOLln1-27-A04"
                     /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
                     /lab_host="Top10F'"
                     /clone_lib="L18POOLln1"
                     /note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996). Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
ORIGIN

Query Match   51.6%; Score 619; DB 6; Length 619;
Best Local Similarity 100.0%; Pred. No. 1.8e-140;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   28 AGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTTATCGGTATTTAACTTTTCTT 87
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   619 AGGGCAAGGGGATGCAAACAATACAAAAATCAAAAGCTTATCGGTATTTAACTTTTCTT 560

Qy   88 TCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTATTTTTACATTTGTCCTGATCTG 147
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   559 TCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTATTTTTACATTTGTCCTGATCTG 500

Qy   148 CTTCATGAAATCCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 207
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   499 CTTCATGAAATCCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 440

Qy   208 CAACTCTTATCAGGGAGGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTGCGTC 267
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439 CAACTCTTATCAGGGAGGCGAACTGCTCATTTCTGCCTACTTCTTTCCCTTGCGTC 380

Qy   268 ATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAG 327
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379 ATGTGTACTACAAAATAGTCATTGCATGCAATGGTGAGGCCCGCAATTAGGGAAAAGAG 320

Qy   328 CTCTGGAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTCATTATTTTGTCCACA 387
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319 CTCTGGAAGCCCACTTTGCCATCTCACACTGGTCCAGGTCCTTCATTATTTTGTCCACA 260

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6701084"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_128"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgcctcggcc);Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >2 kb
size fraction (other fractions present in NIH_MGC_126 and
NIH_MGC_127). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."
ORIGIN

Query Match   51.7%; Score 619.4; DB 5; Length 662;
Best Local Similarity 99.8%; Pred. No. 1.4e-140;
Matches 620; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy   1 GGAACTAAAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624 GAAACTAAAAAGAACTTATTATTGAGGGCAAGGGGATGCAAACAATACAAAAATCAA 565

Qy   61 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 AAGCTTATCTGGTATTTAACTTTTCTTTCTCTTCTGCTTGTCAAATGAGAGTTAGATTTTATT 505

Qy   121 TTTACATTTGTCCTAAGTGTCCTGATCTGCTGCTGCTGGGGAAGCTGTGGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 TTTACATTTGTCCTAAGTGTCCTGATCTGCTGCTGCTGGGGAAGCTGTGGG 445

Qy   181 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGGCTGCTCATT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444 GCAGATTCCTTAAGCGACCCTTTGGGACAACTCTTATCAGGGAGGAGGAGGCTGCTCATT 385

Qy   241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGACTACAAAATAGTCATTGCATGCAATG 325

Qy   301 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 GTGAGGCCCGCAATTAGGGAAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCACACTGG 265

Qy   361 TCCAGGTCCTTCATTATTTTGTCCACAGCCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 TCCAGGTCCTTCATTATTTTGTCCACAGCCCAGAGGGTCTTTTGATTTTCCAAAAATCCA 205

Qy   421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCCTTGTTAAGTAGCCTTTATCCCCA 145

Qy   481 GCGAATTGTGAAAATGTAAACATCATGGTTCATTGAGATGGCATT 540
          |||||||||||||||||||||||||||||||||||||||||||||
Db   144 GCGAATTGTGAAAATGTAAACATCATGGTTCATTGAGATGGCATT 85

Qy   541 TTGGTGTGGTCCGTGAAGCCTTGGCCGGAGGCGTGGGCGGCGAGCTGGGCGAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 TTGGTGTGGTCCGTGAAGCCTTGGCCGGAGGCGTGGGCGGCGAGCTGGGCGAG 25

Qy   601 CTGGACGCGGGGCGGGAGAGGC 621
          ||||||||||||||||||||||
Db   24 CTGGACGCGGGGCGGGAGAGGC 4

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Qy   388  GCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTTCCATGAGTACTCTC  447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259  GCCAGAGGGTCTTTTTGATTTTCCAAAAATCCAGGGAACTCCTTTTTCCATGAGTACTCTC  200

Qy   448  AGGTCCTCCTTTGTTAAGTAGCCCTTTATCCCCAGCCGAATTTGTGAAATGTAAACATCATG 507
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199  AGGTCCTCCTTTGTTAAGTAGCCCTTTATCCCCAGCCGAATTTGTGAAATGTAAACATCATG 140

Qy   508  GTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCTTGGCC   567
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139  GTTTCCATGGCGTGTTCCATTTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCTTGGCC   80

Qy   568  GAGGCCGGCGCGGACGCTGGGCGAGCTGGGCGAGCTGGGCGGGCGCGGGGGCGGAGGCGCGAGCGC 627
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   79   GAGGGCGGCGGCGACGCTGGGCGAGCTGGGCGAGCTGGGCGGGCGCGGGGGCGGAGGCGCGAGCGC 20

Qy   628  GGCGGGCTGTGCGCCTTCC  646
          |||||||||||||||||||
Db   19   GGCGGGCTGTGCGCCTTCC  1
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Job time : 3779 secs